

GenCore version 5.1.6  
(c) 1993 - 2003 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 19:16:44 ; Search time 1433 Seconds

(without alignments)  
214.734 Million cell updates/sec

Title: US-09-581-500b-14

Perfect score: 19  
Sequence: 1 cgctctgattccctgctctg 19

Scoring table: IDENTITY\_NUC

gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:

32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: em\_estba:\*

2: em\_estrum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estoy:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_estl:\*

10: gb\_est2:\*

11: gb\_htc1:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estrun:\*

16: em\_estcom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fut:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rod:\*

## ALIGNMENTS

RESULT 1  
BG347460  
LOCUS BG347460 522 bp mRNA linear EST 28-FEB-2001  
DEFINITION Gab8tail-x1 NICHD XGC Emb2 Xenopus laevis cDNA clone IMAGE:4404381  
3', similar to SWI NOPA\_YEAST P377838 NUCLEOULAR PROTEIN NOPA ;, mRNA  
sequence.  
ACCESSION BG347460.1 GI:13167884  
VERSION EST  
KEYWORDS  
SOURCE  
ORGANISM Xenopus laevis  
REFERENCE  
AUTHORS Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Page,D.  
, Martin,J., Wyllie,T., Underwood,R., Theissing,B., Bowers,Y., Person,  
, Gibbons,M., Harvey,N., Ritter,B., Jackson,Y., McCann,R.,  
Waterston,R. and Wilson,R.  
TITLE WashU Xenopus EST project, 1999  
JOURNAL Unpublished (1999)  
COMMENT Contact: Sandy Clifton, Ph.D.  
WashU Xenopus EST project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1801  
Email: est@watson.wustl.edu  
Library constructed by Life Technologies. DNA Sequencing by:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	17.4	91.6	522	12	BG347460
2	17.4	91.6	1039	9	AU050798
C	17.4	91.6	1101	17	AU309309
4	17	89.5	250	17	AZ2248177
5	17	89.5	250	17	AZ039338
C	6	89.5	772	12	RP01-23-2
					BF627795
					RVSM6000

FEATURES	Location/Qualifiers	RESULT 3
SOURCE	1. organism="Xenopus laevis" /db_xref="taxon:3355" /clone_id="IMAGE:4404381"	CNS04VNO/c
BASE COUNT	95 a	CNS04VNO
ORIGIN	150 c	Tetraodon nigroviridis
Query Match	91.6%; Score 17.4; DB 12; Length 522;	1101 bp
Best Local Similarity	94.7%; Pred. No. 1.8e+03; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	linear
DEFINITION	Tetraodon nigroviridis genome survey sequence T3 end of clone 01019 of library A from Tetraodon nigroviridis, genomic survey sequence.	GSS 24-MAY-2000
VERSION	AJ209309	
SOURCE	GSS: genome survey sequence.	
ORGANISM	Tetraodon nigroviridis.	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Noteleosteii; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon	
AUTHORS	1 (bases 1 to 1101) Roest-Crollius,H., Jajillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Brottier,P., Quettier,F., Saurin,W. and Weissenbach,J.	
KEYWORDS	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence	
COMMENT	Unpublished	
RESULT 2		
LOCUS	AUD050798	AUD050798
DEFINITION	1039 bp mRNA linear EST 09-JUN-1999	
VERSION	AUD050798	1039
KEYWORDS	Paralichthys olivaceus	
SOURCE	Paralichthys olivaceus	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Noteleosteii; Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes; Pleuronectoidea; Paralichthyidae; Paralichthys.	
REFERENCE	1 (bases 1 to 1039) Aoki,T.	
AUTHORS	Unpublished (1999)	
JOURNAL	Japanese flounder leukocyte cDNA	
COMMENT	Contact: Takashi Aoki Tokyo University of Fisheries Konan 4-5-7, Tokyo, Minato-ku 108-8477, Japan Tel: 81-3-5463-0689 Fax: 81-3-5463-0690 Email: aoki@tokyo-u-fish.ac.jp	
FEATURES	bastard halibut	
SOURCE	Paralichthys olivaceus	
DEFINITION	olivaceus cDNA clone WH11-23, mRNA sequence.	
VERSION	AUD050798.1	GI:51019251
KEYWORDS	EST.	
SOURCE		
DEFINITION		
VERSION		
KEYWORDS		
RESULT 1		
LOCUS	AUD050798	AUD050798
DEFINITION	1039 bp mRNA linear EST 09-JUN-1999	
VERSION	AUD050798	1039
KEYWORDS	Paralichthys olivaceus	
SOURCE	Paralichthys olivaceus	
DEFINITION	olivaceus cDNA clone WH11-23, mRNA sequence.	
VERSION	AUD050798.1	GI:51019251
KEYWORDS	EST.	
SOURCE		
DEFINITION		
VERSION		
KEYWORDS		
RESULT 4		
LOCUS	AZ248177	AZ248177
DEFINITION	RPCI-23-39M14.TV RPCI-23 Mus musculus genomic clone RPCI-23-39M14, DNA sequence.	187 bp
VERSION	AZ248177	
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 187) Zhao,S., Nieman,W., Feldblum,T., Malek,J., Shatsman,S., Akinret,B., Levin,C.M., McGinn,S., Tsengye,G., Geer,K., Kroli,M., de Jong,P., and Fraser,C.M.	
TITLE	Mouse BAC End Sequences from Library RPCI-23	



/clone="HWSME005N04F"

/clone 118="Hordeum vulgare seedling shoot EST library"

HtCDNA002 (Dehydrated stress)"

/tissue\_type="Seedling shoot"

/lab\_host="TJCU21"

/note="Vector: lambdaZP; Site\_1: EcoRI; Site\_2: XbaI;

Seeds were surface sterilized then germinated under axenic

conditions in the dark at room temperature on filter paper

with water, mycillin and cefotaxime in covered

crystallization dishes. Five-day old seedlings were

incubated at 90% RH for 24 hr. Shoots were then harvested,

total RNA was prepared, poly(A) RNA was purified, one

primary unamplified cDNA library was made, 600000 pfu were

in vivo excised to give pluecscript SK(-) cDNA phagemids.

These steps were performed in the TJ Close laboratory at

the University of California, Riverside (Choi, Close,

Fenton). Phagemids were plated and picked at the Clemson

University Genomics Institute (CUGI) (Begun, Palmer, Frisch, Atkins and Wing).

Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).

The sequence has been trimmed to remove vector sequence

and contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and

sequence analysis see

<http://www.genome.clemson.edu/projects/barley>. To order

this clone see <http://www.genome.clemson.edu/orders> Also

see Close TJ, Wing R, Kleinhofs A, Wise R (2001)

Genetically and physically anchored EST resources for

barley genomics. Barley Genetics Newsletter 31:29-30.

(<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)

BASE COUNT 294 a 140 c 229 g 109 t

ORIGIN

and the oligo-dT track served to identify it as a clone from the normalized rat heart pool library cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics ([www.resgen.com](http://www.resgen.com))

Seq primer: M13 Forward

POVX-Yes

FEATURES

SOURCE

1. .256

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db\_xref="Raxxon:10116"

/clone\_id="UI-R-DKO-cdm-a-07-0-UI"

/dev\_stage="ADULT"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="UI-R-DKO"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified

polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-DKO

library is a subtracted library derived from a mixture of

five individually tagged normalized rat libraries: brain-nRBP (20%), heart-nRBP (20%), kidney-nRBP (20%),

aorta-nRBP (20%), and placenta-nRBP (20%). Each original

library was constructed from a mixture of equal amounts of

RNA from seven different developmental time-points:

embryonic day 17, embryonic day 19, embryonic day 21,

adult day 1, adult day 12, adult day 75, and adult day

200. (Exception: the aorta pool does not contain embryonic

day 17 RNA and the placenta pool contains only the three

embryonic stages). Each library was normalized

individually according to the procedure described by

Bonaldo, Lennon & Soares (Genome Research 6:

791-806, 1996). For construction of the DKO subtracted

library, plasmid DNA from each of the five individually

tagged normalized libraries was mixed in the proportions

specified above and electroporated into competent bacteria

for production of single-stranded circular DNA

representing the pool of libraries. Single-stranded

circular DNA representing these five normalized libraries

was then used as a tracer in a subtractive hybridization

template preparation comprising: a) a set of about 1,000

arrayed clones from each of the five non-normalized

libraries of brain (CT05), heart (CS05), kidney (CWS05),

aorta (CW05), and placenta (CX05). The resulting pool of

approximately 5,000 clones represented about 33.3% of the

final driver population. A set of about 2,000 arrayed

clones from each of the five normalized libraries of brain

(CT0), heart (CS0), kidney (CU0), aorta (CW0), and

placenta (CX0). The resulting pool of about 10,000 clones

represented about 66.6% of the final driver population.

TAG LIB=UI-R-DKO

TAG TISSUE=rat heart pool

TAG SEQ=ATAGATACAC

BASE COUNT 79 a 36 c 92 g 49 t

ORIGIN

Query Match 86.3%; Score 16.4; DB 13; length 256;

Best Local Similarity 94.4%; Pred. No. 3.9e+03; Mismatches 17; Conservative 0; Indels 0; Gaps 0;

QV 2 GCTGTGATCCGCTCTG 19

Db 188 GCTCTGTTCTGCCTG 171

RESULT 8

AA88460 LOCUS AA88460

DEFINITION aa21b02.s1 Soares NFL\_T\_GBC S1 Homo Sapiens cDNA clone IMAGE:1467435 3' similar to TR:Q1638 Q91638 TAIL-SPECIFIC THYROID

ACCESSION AA88460

VERSION AA88460.1 GI:2394841

KEYWORDS EST.

REFERENCE	SOURCE
JOURNAL	Homo sapiens
COMMENT	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 - (bases 1 to 259)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
FEATURES	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), tumor Gene Index
source	Unpublished (1997)
CONTACT	Contact: Robert Strausberg, Ph.D.
EMAIL	Email: cgsbsr@mail.nih.gov
IMAGE	This clone is available royalty-free through LINTL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
IMAGE ID	1
IMAGE URL	http://www.ncbi.nlm.nih.gov/ncicgap.
IMAGE CONSORTIUM	Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand	Seq primer: -40m13 fwd. ER from Amersham
High quality sequence stop: 1.	Location/Qualifiers
1..259	
ORGANISM	/organism="Homo sapiens"
DB_XREF	/db_xref="taxon:9606"
CLONE	/clone="IMage:1467435"
CLONE LIB	/clone_lib="Soares_NFL_T_GBC_S1"
LAB HOST	/lab_host="DH10B"
NOTE	"Organ: pooled; vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plamid DNA from three normalized libraries (fetal lung NBL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. Following RAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 29480-302087, 682632-687239, 72648-728711, and 73909-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT	50 a 93 c 57 g 59 t
ORIGIN	
QUERY MATCH	86.3%; Score 16.4; DB 9; Length 259;
BEST LOCAL SIMILARITY	94.4%; Pred. No. 4e+03;
MATCHES	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
VERSION	2 GCTCTGATTCCTGCTG 19
QY	42 GCTCTGATTCCTGCTG 59
DB	.
RESULT 9	
LOCUS	BB551260 267 bp mRNA linear EST 12-DEC-2000
DEFINITION	UI-R-CO-ig-e-05-0-UI-R1 UI-R-CO Rattus norvegicus cDNA clone
ACCESSION	UI-R-CO-ig-e-05-0-UI 5', mRNA sequence.
VERSION	BB551260.1 GI:11660990
KEYWORDS	EST.
REFERENCE	Rattus norvegicus
AUTHORS	Rattus norvegicus
ORGANISM	Rattus norvegicus
COMMENT	Rattus norvegicus; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 - (bases 1 to 267)
AUTHORS	Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE	Normaliziation and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
MEDLINE	9704477
COMMENT	Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Echstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
FEATURES	
source	E-mail: msoares@blue.weeg.uiowa.edu
COMMENT	cDNA library Preparation: R.B. Soares Lab Clone distribution: This clone will be available through Research Genetics (www.rsgen.com) This clone is also available through the I.M.A.G.E. Consortium at LINTL (info@image.lnl.gov). IMAGE ID= 1774202
REFERENCE	Seq primer: M13 Forward.
JOURNAL	Location/Qualifiers
COMMENT	1..267
FEATURES	
source	/organism="Hattus norvegicus"
STRAIN	/strain="Sprague-Dawley"
DB_XREF	/db_xref="taxon:1016"
CLONE	/clone="UI-R-CO-ig-e-05-0-UI"
CLONE_LIB	/clone_lib="UI-R-CO"
DEV_STAGE	/dev_stage="adult"
LAB_HOST	/lab_host="DH10B (Life Technologies)"
NOTE	"vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-11 library is a subtracted library derived from the UI-R-11 and UI-R-EL1 libraries. The UI-R-11 library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-EL1 library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18 day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified cDNA inserts from a pool of UI-R-11 and UI-R-EL1 clones from which 3, ESRs had been derived was used as a driver in a hybridization with the pooled UI-R-11 and UI-R-EL1 library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 5: 791-806, 1996)." (Bonaldo, Lennon and Soares, Genome Research 5: 791-806, 1996)
BASE COUNT	56 a 82 c 52 g 77 t
ORIGIN	
QUERY MATCH	86.3%; Score 16.4; DB 12; Length 267;
BEST LOCAL SIMILARITY	94.4%; Pred. No. 4e+03;
MATCHES	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
VERSION	2 GCTCTGATTCCTGCTG 19
QY	Db 219 GCTCTGATTCCTGCTG 236
DB	
RESULT 10	
LOCUS	BB237395 292 bp mRNA linear EST 03-MAY-2002
DEFINITION	TA05017F05P Tab0505 Triticum aestivum cDNA clone Tab05017F05P, mRNA sequence.
ACCESSION	BB237385
VERSION	BB237385.1 GI:20433261
KEYWORDS	EST.
SOURCE	bread wheat.
ORGANISM	Triticum aestivum
COMMENT	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Dillopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.
REFERENCE	1 - (bases 1 to 292)
AUTHORS	Cloutier, S.
TITLE	Wheat functional genomics - Glenlea developing seeds cDNA libraries
JOURNAL	Unpublished (2002)
COMMENT	Contact: Dr. Sylvie Cloutier Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9 Tel: (204) 982-2340





## ORIGIN

Search completed: June 21, 2003, 20:20:28  
Job time : 1437 secs

Query Match 86.3%; Score 16.4; DB 12; Length 392;  
Best Local Similarity 94.4%; Pred. No. 4.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCTTGATTCCTGCTCT 18  
Db 95 CGCTTGATTCCTGCTCT 112

RESULT 15  
BF086663/c  
LOCUS BF086663 CM0-GN0079-150900-547-004 GN0079 Homo sapiens cDNA, mRNA sequence.  
ACCESSION BF086663  
VERSION BF086663.1 GI:10892373  
KEYWORDS EST,  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 392)  
Dias, E., Garcia Correa, R., Verissst-Almeida, S., Briones, M.R.,  
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,  
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,  
Brunstein, A., Carvalho, P.S., Bucher, P., Jongeneel, C.V., O'Hare,  
, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and  
Simpson, A.J.

TITLE shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-270422  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM0-GN0079-15090077-c04&t3=2000-09-15&t4=1>)

seq primer: puc 18 forward  
High quality sequence start: 39  
High quality sequence stop: 392.

## FEATURES

## Source

1. 392  
/organism="Homo sapiens"  
/db\_xref="txon.9606"  
/clone\_lib="GN0079"  
/dev\_stage="Adult"  
/note="Organ: placenta normal; Vector: puc18; Site\_1: Small  
; Site\_2: Small; A mini-library was made by cloning  
products derived from ORESTES PCR (U.S. Letters Patent  
application No. 196,716 - Ludwig Institute for Cancer  
Research) profiles into the pUC 18 vector. Reverse  
transcription of tissue mRNA and cDNA amplification were  
performed under low stringency conditions."

## ORIGIN

Query Match 86.3%; Score 16.4; DB 12; Length 392;  
Best Local Similarity 94.4%; Pred. No. 4.5e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCCTGCTCT 19  
Db 39 GCTCTGATTCCTGCTCT 22

Copyright (c) 1993 - 2003 Compugen Ltd.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 19:56:29 ; Search time 121 Seconds

(without alignments)

230.422 Million cell updates/sec

Title: US-09-581-500B-14

Scoring table: IDENTITY NUC

GapOp 10.0 , GapExt 1.0

Searched: 104219 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA,\*

1: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq:\*

2: /cgn2\_6/prodata/2/pubpna/pct\_NEW\_PUB.seq:\*

3: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq:\*

4: /cgn2\_6/prodata/2/pubpna/US07\_PUBCOMB.seq:\*

5: /cgn2\_6/prodata/2/pubpna/pctUS\_PUBCOMB.seq:\*

6: /cgn2\_6/prodata/2/pubpna/US08\_NEW\_PUB.seq:\*

7: /cgn2\_6/prodata/2/pubpna/US08\_PUBCOMB.seq:\*

8: /cgn2\_6/prodata/2/pubpna/US09\_NEW\_PUB.seq:\*

9: /cgn2\_6/prodata/2/pubpna/US09\_PUBCOMB.seq:\*

10: /cgn2\_6/prodata/2/pubpna/US10\_NEW\_PUB.seq:\*

11: /cgn2\_6/prodata/2/pubpna/US10\_PUBCOMB.seq:\*

12: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq:\*

13: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

14: /cgn2\_6/prodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	16.4	86.3	1769	10	US-09-728-952-95	Sequence 95, Appl
2	16.4	86.3	2550	9	US-10-028-072-59	Sequence 59, Appl
3	16.4	86.3	2550	9	US-10-123-049-59	Sequence 59, Appl
4	15.4	86.3	2550	9	US-10-123-904-59	Sequence 59, Appl
5	16.4	86.3	2550	9	US-10-142-470-59	Sequence 59, Appl
6	16.4	86.3	2550	9	US-10-143-114-59	Sequence 59, Appl
7	16.4	86.3	2550	9	US-10-176-918-59	Sequence 59, Appl
8	16.4	86.3	2550	9	US-10-176-921-59	Sequence 59, Appl
9	16.4	86.3	2550	9	US-10-137-865-59	Sequence 59, Appl
10	16.4	86.3	2550	9	US-10-110-474-59	Sequence 59, Appl
11	16.4	86.3	2550	9	US-10-142-431-59	Sequence 59, Appl
12	16.4	86.3	2550	9	US-10-143-114-59	Sequence 59, Appl
13	15.4	86.3	2550	9	US-10-140-002-59	Sequence 59, Appl
14	16.4	86.3	2550	9	US-10-142-419-59	Sequence 59, Appl
15	16.4	86.3	2550	9	US-10-123-262-59	Sequence 59, Appl
16	16.4	86.3	2550	9	US-10-142-423-59	Sequence 59, Appl
17	16.4	86.3	2550	9	US-10-121-050-59	Sequence 59, Appl
18	16.4	86.3	2550	9	US-10-141-755-59	Sequence 59, Appl
19	16.4	86.3	2550	9	US-10-143-032-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1

US-09-728-952-95

; Sequence 95, Application US/09728952

; Patent No. US2002011302A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wang, Dunrui

; APPLICANT: Yamazaki, Vicki

; APPLICANT: Urvat, Manisha L.

; APPLICANT: Domancic, Radoje T.

; TITLE OF INVENTION: No. US2002011302A1el Nucleic Acids and

; FILE REFERENCE: 739

; CURRENT APPLICATION NUMBER: US/09728,952

; NUMBER OF SEQ ID NOS: 101

; SOFTWARE: pt\_FL\_genes Version 2.0

; SEQ ID NO: 95 ; LENGTH: 1769

; TYPE: DNA

; ORGANISM: Homo sapiens

; FRUITFUL:

; NAME/KEY: CDS

; LOCATION: (282)..(1769)

US-09-728-952-95

Query Match 86.3%; Score 16.4; DB 10; Length 1769;

Best Local Similarity 94.4%; Pred. No. 80;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTGCTGATCTCTCTCTG 19

Db 424 GCTCGTGTGATCTGCTG 441

RESULT 2

US-10-028-072-59

Sequence 59, Application US/10028072  
 Publication No. US20030004311A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Desnoyers, Lug  
 APPLICANT: Filvaroff, Eileen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurley, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Wattanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang

TITLE OF INVENTION:  
 FILE REFERENCE:  
 CURRENT APPLICATION NUMBER: US/10/028,072  
 CURRENT FILING DATE: 2003-12-19  
 PRIOR APPLICATION NUMBER: 60/049911  
 PRIOR FILING DATE: 1997-05-18  
 PRIOR APPLICATION NUMBER: 60/056974  
 PRIOR FILING DATE: 1997-05-26  
 PRIOR APPLICATION NUMBER: 60/059113  
 PRIOR FILING DATE: 1997-05-17  
 PRIOR APPLICATION NUMBER: 60/059115  
 PRIOR FILING DATE: 1997-05-17  
 PRIOR APPLICATION NUMBER: 60/059117  
 PRIOR FILING DATE: 1997-05-17  
 PRIOR APPLICATION NUMBER: 60/059122  
 PRIOR FILING DATE: 1997-05-17  
 PRIOR APPLICATION NUMBER: 60/059184  
 PRIOR FILING DATE: 1997-09-19  
 PRIOR APPLICATION NUMBER: 60/059263  
 PRIOR FILING DATE: 1997-09-18  
 PRIOR APPLICATION NUMBER: 60/059352  
 PRIOR FILING DATE: 1997-09-19  
 PRIOR APPLICATION NUMBER: 60/059588  
 PRIOR FILING DATE: 1997-09-19  
 PRIOR APPLICATION NUMBER: 60/059836  
 PRIOR FILING DATE: 1997-09-24  
 PRIOR APPLICATION NUMBER: 60/062250  
 PRIOR FILING DATE: 1997-09-19  
 PRIOR APPLICATION NUMBER: 60/062285  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/062287  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/062814  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/062816  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/063045  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/063327  
 PRIOR FILING DATE: 1997-10-27  
 PRIOR APPLICATION NUMBER: 60/063329  
 PRIOR FILING DATE: 1997-10-31  
 PRIOR APPLICATION NUMBER: 60/063127  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/063561  
 PRIOR FILING DATE: 1997-10-28  
 PRIOR APPLICATION NUMBER: 60/063704  
 PRIOR FILING DATE: 1997-10-29  
 PRIOR APPLICATION NUMBER: 60/063733  
 PRIOR FILING DATE: 1997-10-29  
 PRIOR APPLICATION NUMBER: 60/063735  
 PRIOR FILING DATE: 1997-10-29  
 PRIOR APPLICATION NUMBER: 60/063738  
 PRIOR FILING DATE: 1997-10-29  
 PRIOR APPLICATION NUMBER: 60/063755  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/064248  
 PRIOR FILING DATE: 1997-11-03  
 PRIOR APPLICATION NUMBER: 60/064809  
 PRIOR FILING DATE: 1997-11-07  
 PRIOR APPLICATION NUMBER: 60/065186  
 PRIOR FILING DATE: 1997-11-12  
 PRIOR APPLICATION NUMBER: 60/065846  
 PRIOR FILING DATE: 1997-11-17  
 PRIOR APPLICATION NUMBER: 60/066364  
 PRIOR FILING DATE: 1997-11-21  
 PRIOR APPLICATION NUMBER: 60/066453  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/066511  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/066770  
 PRIOR FILING DATE: 1997-11-24  
 PRIOR APPLICATION NUMBER: 60/069212  
 PRIOR FILING DATE: 1997-12-11  
 PRIOR APPLICATION NUMBER: 60/069278  
 PRIOR FILING DATE: 1997-12-11  
 PRIOR APPLICATION NUMBER: 60/069334  
 PRIOR FILING DATE: 1997-12-11  
 PRIOR APPLICATION NUMBER: 60/069694  
 PRIOR FILING DATE: 1997-12-16  
 PRIOR APPLICATION NUMBER: 60/072320  
 PRIOR FILING DATE: 1998-01-23  
 PRIOR APPLICATION NUMBER: 60/073612  
 PRIOR FILING DATE: 1998-02-04  
 PRIOR APPLICATION NUMBER: 60/074086  
 PRIOR FILING DATE: 1998-02-09  
 PRIOR APPLICATION NUMBER: 60/074092  
 PRIOR FILING DATE: 1998-02-09  
 PRIOR APPLICATION NUMBER: 60/077991  
 PRIOR FILING DATE: 1998-03-12  
 PRIOR APPLICATION NUMBER: 60/079663  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/079294  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079663  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/079728  
 PRIOR FILING DATE: 1998-03-27  
 PRIOR APPLICATION NUMBER: 60/080165  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/081203  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081229  
 PRIOR FILING DATE: 1998-04-09  
 PRIOR APPLICATION NUMBER: 60/081695  
 PRIOR FILING DATE: 1998-04-14  
 PRIOR APPLICATION NUMBER: 60/081817  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/081818  
 PRIOR FILING DATE: 1998-04-15  
 PRIOR APPLICATION NUMBER: 60/082999  
 PRIOR FILING DATE: 1998-04-24  
 PRIOR APPLICATION NUMBER: 60/083322  
 PRIOR FILING DATE: 1998-04-28  
 PRIOR APPLICATION NUMBER: 60/083545  
 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084637  
 PRIOR FILING DATE: 1998-05-07



Qy 2 GCTCTGATTCCTGCTCTG 19  
 US-10-140-470-59  
 ; Sequence 59, Application US/10140470  
 ; Publication No. US20030022331A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.

ApPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Denoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watamabe, Colin K  
 APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C160

CURRENT APPLICATION NUMBER: US/10/140,470

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 59

LENGTH: 2550

TYPE: DNA

ORGANISM: Homo Sapien

US-10-175-746-59

RESULT 5

Qy 2 GCTCTGATTCCTGCTCTG 19  
 US-10-175-746-59  
 ; Sequence 59, Application US/10175746  
 ; Publication No. US20030022725A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Denoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watamabe, Colin K  
 APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C353

CURRENT APPLICATION NUMBER: US/10/175,746

CURRENT FILING DATE: 2002-05-19

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 59

LENGTH: 2550

TYPE: DNA

ORGANISM: Homo Sapien

US-10-175-746-59

RESULT 6

Qy 2 GCTCTGATTCCTGCTCTG 19  
 US-10-175-746-59  
 ; Sequence 59, Application US/10175746  
 ; Publication No. US20030022725A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Denoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watamabe, Colin K  
 APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C353

CURRENT APPLICATION NUMBER: US/10/175,746

CURRENT FILING DATE: 2002-05-19

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 59

LENGTH: 2550

TYPE: DNA

ORGANISM: Homo Sapien

US-10-175-746-59

RESULT 7

Qy 2 GCTCTGATTCCTGCTCTG 19  
 US-10-176-918-59  
 ; Sequence 59, Application US/10176918  
 ; Publication No. US200300227275A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Denoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary B.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watamabe, Colin K  
 APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C382

CURRENT APPLICATION NUMBER: US/10/176,918

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 59

LENGTH: 2550

TYPE: DNA

ORGANISM: Homo Sapien

US-10-176-918-59

RESULT 8

Qy 2 GCTCTGATTCCTGCTCTG 19  
 US-10-176-918-59  
 ; Sequence 59, Application US/10176921  
 ; Publication No. US200300227275A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura

APPLICANT: Denoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary B.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watamabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C382

CURRENT APPLICATION NUMBER: US/10/176,921

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 59

LENGTH: 2550

TYPE: DNA

ORGANISM: Homo Sapien

US-10-176-918-59

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10  
 US-10-140474-59  
 ; Sequence 59, Application US/10140474  
 ; Publication No. US2003003215621

GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watarabe, Colin K

APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watarabe, Colin K

Query Match 86.3%; Score 16.4; DB 9; Length 2550;  
 Best Local Similarity 94.4%; Pred. No. 80; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCTCTGATCCCTGCTG 19  
 Db 438 GCTCTGATCCCTGCTG 455

RESULT 9  
 US-10-137865-59  
 ; Sequence 59, Application US/10137865

GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watarabe, Colin K

APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watarabe, Colin K

Query Match 86.3%; Score 16.4; DB 9; Length 2550;  
 Best Local Similarity 94.4%; Pred. No. 80; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCTCTGATCCCTGCTG 19  
 Db 438 GCTCTGATCCCTGCTG 455

RESULT 11  
 US-10-142431-59  
 ; Sequence 39, Application US/10142431

GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Stewart, Victoria  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watarabe, Colin K

APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Stewart, Victoria  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watarabe, Colin K

Query Match 86.3%; Score 16.4; DB 9; Length 2550;  
 Best Local Similarity 94.4%; Pred. No. 80; Length 2550;

RESULT 12

Query Match 86.3%; Score 16.4; DB 9; Length 2550;  
 Best Local Similarity 94.4%; Pred. No. 80;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCTCTGATCCCTGCTG 19  
 Db 438 GCTCTGATCCCTGCTG 455

US-10-143-114-59

Sequence 59, Application US/10143114  
 Publication No. US20030036180A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeGeorge, Laura  
 APPLICANT: Destroyer, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godtowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Stewart, Victoria  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanaabe, Colin K.  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 TIME OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3330R1C211  
 CURRENT APPLICATION NUMBER: US/10/143,114  
 CURRENT FILING DATE: 2002-05-09  
 Prior Application removed - See Palm or File Wrapper  
 NUMBER OF SEQ ID NOS: 550  
 LENGTH: 2550  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-143-114-59

RESULT 13

Query Match 86.3%; Score 16.4; DB 9; Length 2550;  
 Best Local Similarity 94.4%; Pred. No. 80;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCTCTGATCCCTGCTG 19  
 Db 438 GCTCTGATCCCTGCTG 455

US-10-140-002-59

Sequence 59, Application US/10140,002  
 Publication No. US2003003623A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeGeorge, Laura  
 APPLICANT: Destroyer, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanaabe, Colin K.  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 TIME OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3330R1C244  
 CURRENT APPLICATION NUMBER: US/10/142,419  
 CURRENT FILING DATE: 2002-05-10  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 550  
 SEQ ID NO 59  
 LENGTH: 2550  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-142-419-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;

Best Local Similarity 94.4%; Pred. No. 80; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATGATCTGCTCG 19  
Db 438 GCTCTGATGATCTGCTCG 455

RESULT 15

US-10-123-262-59

; Sequence 59, Application US/10123262  
; Publication No. US20030049816A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beersini, Maureen

; APPLICANT: DeGeorge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filivarooff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smuth, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tunas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TIME OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TIME OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3350R1C38

; CURRENT APPLICATION NUMBER: US/10-123, 262

; CURRENT FILING DATE: 2002-04-15

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 59

; LENGTH: 2550

; TYPE: DNA

; ORGANISM: Homo Sapien

; US-10-123-262-59

Query Match 86.3%; Score 16.4; DB 9; Length 2550;

Best Local Similarity 94.4%; Pred. No. 80; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATGATCTGCTCG 19  
Db 438 GCTCTGATGATCTGCTCG 455

Search completed: June 21, 2003, 21:12:24  
Job time : 122 secs

Copyright (c) 1993 - 2003 Compugen Ltd.

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 19:32:08 ; Search time 63 Seconds  
(without alignments)

92.490 Million cell updates/sec

Title: US-09-581-500B-14  
Perfect score: 19  
Sequence: 1 cgctctgattccgtctg 19  
Scoring table: IDENTITY\_NUC  
GapOp 10.0 , GapExt 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
Issued\_Patents\_NA:  
1: /cgn2\_6/procdata/2/ina/5A\_COMB.seq:  
2: /cgn2\_6/procdata/2/ina/5B\_COMB.seq:  
3: /cgn2\_6/procdata/2/ina/6A\_COMB.seq:  
4: /cgn2\_6/procdata/2/ina/6B\_COMB.seq:  
5: /cgn2\_6/procdata/2/ina/PCITS\_COMB.seq:  
6: /cgn2\_6/procdata/2/ina/backfile1.seq:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
C 1	15.8	83.2	1200	US-08-096-623A-19
C 2	15.8	83.2	71989	US-09-443-501A-2
C 3	15.8	83.2	246340	US-08-724-3942-20
C 4	15.8	83.2	246340	US-08-724-3942-21
C 5	15.8	83.2	246340	US-08-724-3942-22
C 6	15.4	81.1	1093	US-08-592-126-95
C 7	15.4	81.1	36519	US-08-923-137-2
C 8	15.4	81.1	1800	US-08-919-937-11
C 9	15	78.9	1800	PCT-US93-11310-11
C 10	14.8	77.9	2015	US-08-129-129-7
C 11	14.8	77.9	5232	US-08-972-927-1
C 12	14.8	77.9	7326	US-08-194-468-1
C 13	14.8	77.9	7326	US-09-514-247A-7
C 14	14.8	77.9	7344	US-08-961-739-1
C 15	14.8	77.9	7431	US-09-306-998-2
C 16	14.8	77.9	8147	US-09-514-247A-9
C 17	14.8	77.9	15053	US-09-901-502-3
C 18	14.8	77.9	45716	US-08-965-048-5
C 19	14.8	77.9	45989	US-08-965-048-6
C 20	14.4	75.8	2522	US-09-611-781-1
C 21	14.4	75.8	1272	US-09-611-781-7
C 22	14.4	75.8	1847	US-09-058-389A-9
C 23	14.4	75.8	16053	US-09-611-781-9
C 24	14.4	75.8	2522	US-09-058-389A-1
C 25	14.4	75.8	2522	US-09-611-781-1
C 26	14.4	75.8	3489	US-09-728-323A-1
C 27	14.4	75.8	3489	US-09-728-323A-1

ALIGMENTS

RESULT 1  
US-08-096-623A-19/C  
; Sequence 19, Appli  
; Parent No. 5684238  
; GENERAL INFORMATION:  
; APPLICANT: Brinkhans, Friedhelm L.  
; APPLICANT: Proffitt, John H.  
; APPLICANT: Yarger, James G.  
; APPLICANT: Yen, Ruei-Che B.  
; TITLE OF INVENTION: Biosynthesis of Zeaxanthin and  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Walsh & Katz, Ltd.  
; STREET: 120 S. Riverside Plaza, 22nd Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US-08-096, 623A  
; FILING DATE: 22-JUL-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/805, 061  
; FILING DATE: 09-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/662, 921  
; FILING DATE: 28-FEB-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/562, 674  
; FILING DATE: 03-APR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/525, 551  
; FILING DATE: 18-MAY-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/487, 613  
; FILING DATE: 02-MAR-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gammon, Edward P.  
; REGISTRATION NUMBER: 29, 381  
; REFERENCE/DOCKET NUMBER: AMO-006.1  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 655-1500  
 TELEFAX: (312) 655-1501  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1200 base pairs  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: DNA (genomic)  
 POSITION IN GENOME:  
 MAP POSITION: 1 to 1200  
 UNITS: bp  
 US-08-096-623a-19

RESULT 2  
 US-09-43-501A-2/c  
 ; Sequence 2, Application US/09443501A  
 ; Patent No. 630342  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kosan Biosciences, Inc.  
 ; APPLICANT: Juilien, Bryan  
 ; APPLICANT: Katz, Leonard  
 ; APPLICANT: Kosla, Chaitan  
 ; APPLICANT: Tang, Li  
 ; TITLE OF INVENTION: Recombinant Methods and Materials for Producing  
 ; FILE REFERENCE: 30062-20031.00  
 ; CURRENT APPLICATION NUMBER: US/09/443,501A  
 ; CURRENT FILING DATE: 1999-11-19  
 ; PRIOR APPLICATION NUMBER: US 60/130,560  
 ; PRIOR FILING DATE: 1998-04-22  
 ; PRIOR APPLICATION NUMBER: US 60/122,620  
 ; PRIOR FILING DATE: 1998-03-03  
 ; PRIOR APPLICATION NUMBER: US 60/119,386  
 ; PRIOR FILING DATE: 1998-02-10  
 ; PRIOR APPLICATION NUMBER: US 60/109,401  
 ; PRIOR FILING DATE: 1998-11-20  
 ; NUMBER OF SEQ ID NOS: 22  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 71989  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic construct  
 ; US-09-43-501A-2

Query Match 83.2%; Score 15.8; DB 4; Length 71989;  
 Best Local Similarity 89.5%; Pred. No. 1e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCTCTGATTCTGCTGCTG 19  
 Db 63977 CGCTCTGATTCTGCTG 63959

RESULT 2  
 US-09-43-501A-2/c  
 ; Sequence 2, Application US/09443501A  
 ; Patent No. 630342  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Feder, John N.  
 ; APPLICANT: Krommal, Gregory S.  
 ; APPLICANT: Lauer, Peter M.  
 ; APPLICANT: Ruddy, David A.  
 ; APPLICANT: Thomas, Winson  
 ; APPLICANT: Tsuchihashi, Zenta  
 ; APPLICANT: Wolff, Roger K.  
 ; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1  
 ; TITLE OF INVENTION: Sequences and Antibodies Thereof  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: TOWNSEND and CREW LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: CA

ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/724,394A  
 FILING DATE: 01-OCT-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fitts, Renee A.  
 REGISTRATION NUMBER: 35,136  
 REFERENCE/DOCKET NUMBER: 017957-000100  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-576-0200  
 TELEFAX: 415-576-0300  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 246240 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLogy: not relevant  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..246240  
 OTHER INFORMATION: /note= "HLA-H-CONTIG"

US-08-724-394A-20

Query Match 83.2%; Score 15.8; DB 2; Length 246240;  
 Best Local Similarity 89.5%; Pred. No. 1.1e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCTCTGATTCTGCTGCTG 19  
 Db 161737 CGCTCTGATTCTGCTG 161755

RESULT 4  
 US-08-724-394A-21  
 ; Sequence 21, Application US/08724394A  
 ; Patent No. 5872237  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Feder, John N.  
 ; APPLICANT: Krommal, Gregory S.  
 ; APPLICANT: Lauer, Peter M.  
 ; APPLICANT: Ruddy, David A.  
 ; APPLICANT: Thomas, Winson  
 ; APPLICANT: Tsuchihashi, Zenta  
 ; APPLICANT: Wolff, Roger K.  
 ; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1  
 ; TITLE OF INVENTION: Sequences and Antibodies Thereof  
 ; NUMBER OF SEQUENCES: 31  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: TOWNSEND and CREW LLP  
 ; STREET: Two Embarcadero Center, 8th Floor  
 ; CITY: San Francisco  
 ; STATE: CA

RESULT 3  
 US-08-724-394A-20  
 ; Sequence 20, Application US/08724394A  
 ; Patent No. 5872237  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Feder, John N.  
 ; APPLICANT: Krommal, Gregory S.

COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/724,394A  
 FILING DATE: 01-OCT-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fitts, Renee A.  
 REGISTRATION NUMBER: 35,136  
 REFERENCE/DOCKET NUMBER: 017957-000100  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-576-0200  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 246240 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..246240  
 OTHER INFORMATION: /note= "HLA-H.CONTIG"  
 US-08-724-394A-21  
 INFORMATION FOR SEQ ID NO: 21:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 246240 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..246240  
 OTHER INFORMATION: /note= "HLA-H.CONTIG"  
 US-08-724-394A-22  
 INFORMATION FOR SEQ ID NO: 22:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 246240 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: 1..246240  
 OTHER INFORMATION: /note= "HLA-H.CONTIG"  
 US-08-724-394A-22  
 RESULT 5  
 Sequence 22, Application US/08724394A  
 ; General Information:  
 ; Patent No. 587237  
 ; General Information:  
 ; Applicant: Feder, John N.  
 ; Applicant: Kronmal, Gregory S.  
 ; Applicant: Lau, Peter M.  
 ; Applicant: Ruddy, David A.  
 ; Applicant: Thomas, Winston  
 ; Applicant: Tsuchihashi, Zenta  
 ; Applicant: Wolff, Roger K.  
 ; Title of Invention: Megabase Transcript Map: No. 587237el  
 ; Title of Invention: Sequences and Antibodies Thereto  
 ; Number of Sequences: 31  
 ; Correspondence Address:  
 ; Addressee: TOWNSEND and TOWNSEND and CREW LLP  
 ; Street: Two Embarcadero Center, 8th Floor  
 ; City: San Francisco  
 ; State: CA  
 ; Country: USA  
 ; ZIP: 94106  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent-In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/592,126  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sholtz, Charissa K.  
 REGISTRATION NUMBER: 38,615  
 REFERENCE/DOCKET NUMBER: 4600-0111  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 324-0880  
 TELEFAX: (415) 324-0960  
 INFORMATION FOR SEQ ID NO: 95:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1093 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: G164con.seq  
 US-08-592-126-95  
 Query Match 81.1%; Score 15.4; DB 1; Length 1093;

Best Local Similarity 94.1%; Pred No 97; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCTCTGATTCCTGCTCT 18  
Db 988 GCTCTGATTCCTGCTCT 972

RESULT 7

US-08-923-137-2/c

; Sequence 2, Application US/08923137

; Patent No. 6083116

; GENERAL INFORMATION:

; APPLICANT: Marina, Steven F.

; APPLICANT: Fisher, Krishna J.

; TITLE OF INVENTION: Chimpanzee Adenovirus Vectors

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howson and Howson

; STREET: Spring House Corporate Cntr., P.O. Box 457

; CITY: Spring House

; STATE: Pennsylvania

; COUNTRY: United States of America

; ZIP: 19477

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 07/979,156

APPLICATION NUMBER: US 08/139,937

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, CATHERIN

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-CJ 9370

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-535-9001

FAX: 619-535-8349

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1800 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-139-937-11

Query Match 78.9%; Score 15; DB 1; Length 180;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCTCTGATTCCTGCTCT 16  
Db 1698 GCTCTGATTCCTGCTCT 1684

RESULT 9

PCT-US 93-11310-11/c

; Sequence 11, Application PC/TUS9311310

; GENERAL INFORMATION:

; APPLICANT: BOARD OF REGENTS OF THE UNIVERSITY OF TEXAS SYSTEM

; TITLE OF INVENTION: CELLULAR GENES ENCODING RETINOBLASTOMA-ASSOCIATED PROTEINS

; TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CAMPBELL AND FLORES

; STREET: 4370 LA JOLLA VILLAGE DRIVE

; CITY: SAN DIEGO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11310

FILING DATE: 19-Nov-1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, CATHERIN

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-CJ 9790

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-535-9001

RESULT 8

US-08-139-937-11/c

; Sequence 11, Application US/08139937

; Patent No. 5821070

; GENERAL INFORMATION:

; APPLICANT: LEE, WEN-JWA

; APPLICANT: SHAN, BEI

; TITLE OF INVENTION: CELLULAR GENES ENCODING

; TITLE OF INVENTION: RETINOBLASTOMA-ASSOCIATED PROTEINS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:



Patent No. 5750336  
 GENERAL INFORMATION:  
 APPLICANT: Montminy, Marc R.  
 TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN  
 TITLE OF INVENTION: RESPONSIVE GENES  
 NUMBER OF SEQUENCES: 3  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark  
 STREET: 444 South Flower Street, Suite 2000  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/194,468  
 FILING DATE: 10-FEB-1994  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reiter, Stephen E.  
 REGISTRATION NUMBER: 31,192  
 REFERENCE/DOCKET NUMBER: P41 9672  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (619) 546-4737  
 TELEFAX: (619) 544-9392  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7326 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 1..7323  
 US-08-194-468-1  
 RESULT 13  
 US-09-514-247A-7/C  
 ; Sequence 7, Application US/09514247A  
 ; Patent No. 6365361  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TANABE SEIYAKU CO. LTD.  
 ; APPLICANT: TANIGUCHI, Tomoyasu  
 ; APPLICANT: MITUKAMI, Junko  
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING OR SCREENING AGONIST AND ANTAGONIST TO PPAR  
 ; FILE REFERENCE: TANIGUCHI\_6  
 ; CURRENT APPLICATION NUMBER: US/09/514,247A  
 ; CURRENT FILING DATE: 2000-02-28  
 ; PRIORITY APPLICATION NUMBER: PCT/JP98/13734  
 ; PRIORITY FILING DATE: 1998-08-24  
 ; PRIORITY APPLICATION NUMBER: JP231084/1997  
 ; PRIORITY FILING DATE: 1997-08-27  
 ; NUMBER OF SEQ ID NOS: 10  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 7326  
 Query Match 77.9%; Score 14.8; DB 1; Length 7326;  
 Best Local Similarity 88.9%; Pred. No. 2.3e+02; Mismatches 16; Conservative 0; Indels 0; Gaps 0;  
 Matches 16; Conservatve 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 GCTCTGATTCCTGCTCTG 19  
 Db 3136 GCTCTGACTCTGCTCTG 3119  
 ; US-08-961-739-1  
 RESULT 14  
 US-08-961-739-1/C  
 ; Sequence 1, Application US/08961739A  
 ; Patent No. 6063533  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Montminy, Marc R.  
 ; TITLE OF INVENTION: Methods for Treating Diabetes Mellitus  
 ; FILE REFERENCE: SALK1650-1  
 ; CURRENT APPLICATION NUMBER: US/08/961,739A  
 ; EARLIER FILING DATE: 1997-10-31  
 ; EARLIER APPLICATION NUMBER: US 194,468  
 ; EARLIER FILING DATE: 1994-02-10  
 ; NUMBER OF SEQ ID NOS: 4  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 7326  
 ; TYPE: DNA  
 ; ORGANISM: Mus  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(7326)  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(7326)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-08-961-739-1  
 ; US-09-06-998-2  
 ; Sequence 2, Application US/09306998  
 ; Patent No. 623173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bartel, Paul L.  
 ; APPLICANT: Tavighian, Sean V.  
 ; APPLICANT: Tavighian, Sean V.  
 ; TITLE OF INVENTION: MMSC- An MMAC1 Interacting Protein  
 ; FILE REFERENCE: MMSC2  
 ; CURRENT APPLICATION NUMBER: US/09/306,998  
 ; CURRENT FILING DATE: 1999-05-07  
 ; EARLIER APPLICATION NUMBER: US 60/084,740  
 ; EARLIER FILING DATE: 1998-05-08  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 7431  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LENGTH: 7326  
 Query Match 77.9%; Score 14.8; DB 3; Length 7344;  
 Best Local Similarity 88.9%; Pred. No. 2.3e+02; Mismatches 22; Indels 0; Gaps 0;  
 Matches 16; Conservatve 0; Mismatches 22; Indels 0; Gaps 0;  
 QY 2 GCTCTGATTCCTGCTCTG 19  
 Db 3136 GCTCTGACTCTGCTCTG 3119  
 ; US-09-06-998-2  
 ; Sequence 3, Application US/09306998  
 ; Patent No. 623173  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bartel, Paul L.  
 ; APPLICANT: Tavighian, Sean V.  
 ; TITLE OF INVENTION: MMSC- An MMAC1 Interacting Protein  
 ; FILE REFERENCE: MMSC2  
 ; CURRENT APPLICATION NUMBER: US/09/306,998  
 ; CURRENT FILING DATE: 1999-05-07  
 ; EARLIER APPLICATION NUMBER: US 60/084,740  
 ; EARLIER FILING DATE: 1998-05-08  
 ; NUMBER OF SEQ ID NOS: 72  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 3  
 ; LENGTH: 7431  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LENGTH: 7326

LOCATION: (57) .. (6167)  
us-09-306-998-2

Query Match 77.9%; Score 14.8; DB 4; Length 7431;  
Best Local Similarity 88.9%; Pred. No. 2.4e-02;  
Matches 16; Conservative 0; Mismatches 2;  
Indels 0; Gaps 0;

Qy 2 GCTCTGATTCTGCTG 19  
||| ||||| ||||| |||||  
Db 303 GCTCTGATTCTACTCTG 320

Search completed: June 21, 2003, 20:21:43  
Job time : 65 secs

GenCore version 5.1.6									
Copyright (c) 1993 - 2003 Compugen Ltd.									
Run on: June 21, 2003, 18:29:33 ; Search time 215 Seconds									
(without alignments)									
199.014 Million cell updates/sec									
Title: US-09-581-500B-14	Scoring table: IDENTITY_NUC	Sequence: 1 cgttctgattccgtctg 19	Perfect score: 19	Gapg 10_0 , Gapext 1.0	Searched: 2185239 seqs, 1125999159 residues	Total number of hits satisfying chosen parameters: 4370478	Minimum DB seq length: 0	Maximum DB seq length: 200000000	Post-processing: Minimum Match 0%
Maximum Match 100%	Listing first 45 summaries								
Database :									
N_Geneseq_101002:*									
1: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1980.DAT:*									
2: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1981.DAT:*									
3: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1982.DAT:*									
4: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1983.DAT:*									
5: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1984.DAT:*									
6: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1985.DAT:*									
7: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1986.DAT:*									
8: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1987.DAT:*									
9: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1988.DAT:*									
10: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1989.DAT:*									
11: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1990.DAT:*									
12: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1991.DAT:*									
13: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1992.DAT:*									
14: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1993.DAT:*									
15: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1994.DAT:*									
16: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1995.DAT:*									
17: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1996.DAT:*									
18: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1997.DAT:*									
19: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA1998.DAT:*									
20: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2000.DAT:*									
21: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2001A.DAT:*									
22: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2001B.DAT:*									
23: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2002.DAT:*									
24: /SIDS2/gcdata/geneseq/geneseqn-emb1/NA2002.DAT:*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query Length	DB ID	Description					
1	19	100.0	19	20 AAX88558	Human chromosome 1	XX	XX	XX	XX
2	19	100.0	656	20 AAX88553	Human chromosome 1	XX	XX	XX	XX
3	17	89.5	112460	24 ABK83567	Human cDNA, differ	XX	XX	XX	XX
4	16.4	86.3	502	22 AAF95339	Lung carcinoma cDNA	XX	XX	XX	XX
5	16.4	86.3	511	22 AAF9532	Lung carcinoma cDNA	XX	XX	XX	XX
6	16.4	86.3	857	22 AAH03486	Human cDNA clone (	XX	XX	XX	XX
7	16.4	86.3	1769	24 ABK91976	Human novel polyu	XX	XX	XX	XX
8	16.4	86.3	1873	22 AHI13643	Human cDNA sequenc	XX	XX	XX	XX
9	16.4	86.3	2252	22 AAH16697	Human cDNA sequenc	XX	XX	XX	XX
ALIGNMENTS									
ID: AAX88558	AC: AAX88558;	DT: 10-SEP-1999	XX	DE: Human chromosome 18q YAC clone amplification primer.	KW: Human chromosome 18q; mood disorder; Polymorphic marker; detection; anxiety disorder; trinucleotide repeat expansion; schizophrenia; nucleotide triplet repeat; ss.	XX	XX	XX	XX
OS: Synthetic.	OS: Homo sapiens.	PN: W09932643-A2.	XX	PD: 01-JUL-1999.	PD: 17-DEC-1998; 93W0-EP08543.	XX	PR: 18-DEC-1997; 97GB-0026804.	PR: (VLA&gt;) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.	PR: Del-Favero J, Raemakers P, Van Broeckhoven C; WPI: 1999-418934/35.

PT	Detecting nucleotide triplet repeats in human chromosome 18q
PS	Claim 29; Fig 15b; 87pp; English.
XX	
CC	The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers D18868 and D18897 to identify a human gene associated with a mood disorder or related disorder. AAX8542 to AAX8705 represents human chromosome 18q YAC clones and primers corresponding to them, used in the exemplification of the present invention. YAC clones comprising a portion of the region of human chromosome 18q between markers D18868 and D18879 are used to identify at least one human gene associated with a mood disorder or related disorder. The mood disorder or related disorder is chosen from the Diagnostic and Statistical Manual of Mental Disorders, version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4, 301, 311, 312, 295.70), schizophrenia and related disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3), adjustment disorders (300.XX), and personality disorders (codes 301.XX). Probes derived from genes associated with the mood disorder or related disorder can be used to detect pathological mutations or genetic variations in patients. The methods, probes and antibodies can be used to determine the susceptibility of an individual to a mood disorder or related disorder. The nucleic acids and proteins of the human gene can be used to treat mood disorders and related disorders.
CC	Sequence 19 BP; 1 A; 7 C; 4 G; 7 T; 0 other;
SQ	Query Match 100.0%; Score 19; DB 20; Length 19; Best Local Similarity 100.0%; Pred. No. 17; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CGCTCTGATTCCTGCTG 19
Db	1 CGCTCTGATTCCTGCTG 19
RESULT 2	
AXX8853/C	
ID AAX8853 standard; DNA; 656 BP.	
XX	
AC AAX8853;	
XX	
DT 10-SEP-1999 (first entry)	
DE Human chromosome 18q YAC clone nucleotide sequence #12.	
XX	
KW Human chromosome 18q; mood disorder; polymorphic marker; detection; identification; trinucleotide repeat; expansion; schizophrenia; anxiety disorder; adjustment disorder; personality disorder; nucleotide triplet repeat; ss.	
XX	
OS Homo sapiens.	
XX	
PN WO9932643A2.	
XX	
PD 01-JUL-1999.	
XX	
PP 17-DEC-1998; 98WO-EP08543.	
XX	
PR 18-DEC-1997; 97GB-0026804.	
XX	
PA (VIAA-) VIAMAS INTERUNIVERSITAIR INST BIOTECHNOQ.	
XX	
PI Del-Pavero J, Raeymaekers P, Van Broeckhoven C;	
XX	
DR NBI; 1999-418934/35.	
XX	
PT Detecting nucleotide triplet repeats in human chromosome 18q	
XX	
PS Claim 21; Fig 15a; 87pp; English.	
XX	
PT	
CC	The present invention describes detecting nucleotide triplet repeats in a region of human chromosome 18q disposed between polymorphic markers D18868 and D18897 to identify a human gene associated with a mood disorder or related disorder. AAX8542 to AAX8705 represents human chromosome 18q YAC clones and primers corresponding to them, used in the exemplification of the present invention. YAC clones comprising a portion of the region of human chromosome 18q between markers D18868 and D18879 are used to identify at least one human gene associated with a mood disorder or related disorder. The mood disorder or related disorder is chosen from the Diagnostic and Statistical Manual of Mental Disorders, version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4, 311, 301, 13, 295.70), schizophrenia and related disorders (295, 297.1, 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3), adjustment disorders (300.XX), and personality disorders (codes 301.XX). Probes derived from genes associated with the mood disorder or related disorder can be used to detect pathological mutations or genetic variations in patients. The methods, probes and antibodies can be used to determine the susceptibility of an individual to a mood disorder or related disorder. The nucleic acids and proteins of the human gene can be used to treat mood disorders and related disorders.
CC	Sequence 656 BP; 183 A; 165 C; 208 G; 96 T; 4 other;
SQ	Query Match 100.0%; Score 19; DB 20; Length 656; Best Local Similarity 100.0%; Pred. No. 21; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CGCTCTGATTCCTGCTG 19
Db	533 CGCTCTGATTCCTGCTG 515
RESULT 3	
ARK83567	
ID ARK83567	
XX	
AC ARK83567;	
XX	
DT 14-AUG-2002 (first entry)	
XX	
DE Human cDNA differentially expressed in granulocytic cells #138.	
XX	
KW Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protocol infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; KW cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; Periodontal disease; KW granulocyte activation; chronic inflammation; allergy.	
XX	
OS Homo sapiens.	
XX	
PN WO200228399-12.	
XX	
PD 11-APR-2002.	
XX	
PP 03-OCT-2001; 2001WO-US30821.	
XX	
PR 03-OCT-2000; 2000US-2377189P.	
XX	
PA (GENE-) GENE LOGIC INC.	
XX	
PI Beazier-Barclay Y, Weissman SM, Yamaga S, Vockley J;	
XX	
DR WPI; 2002-435328/46.	
XX	
PT Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity -	
XX	



CC different human tissue cDNA libraries. The invention relates to a method for detecting cDNA encoding an SRT protein, a vector containing cDNA encoding SRT, a host cell transformed with the vector, an isolated SRT polypeptide, and an antibody which binds to SRT. The polynucleotide sequence can be used in gene therapy and is useful in the recombinant production of SRT polypeptides, as a hybridisation probe to screen libraries to isolate cDNAs with sequence identity to SRT polypeptides, to map the gene encoding the SRT polypeptides and analysing genetic disorders, tissue typing and disease tissue detection. The SRT polynucleotide sequences can be used in polymerase chain reaction, screening for new therapeutic molecules and generation of antisense RNA and DNA.

XX SQ Sequence 511 BP; 98 A; 168 C; 119 G; 125 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 511; Best Local Similarity 94.4%; Pred. No. 3.2e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCATGCTCTG 19  
Db 445 GCTCTGATTCATGCTCTG 462

RESULT 6

AAH08486  
XX ID AAH08486 standard; cDNA; 857 BP.  
AC AAH08486;  
XX DT 26-JUN-2001 (first entry)  
XX DE Human cDNA clone (5'-primer) SEQ ID NO:5321.

XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss. Homo sapiens.  
XX OS Homo sapiens.  
XX PN EP1074617-A2.  
XX PD 07-FEB-2001.  
XX PR 28-JUN-2000; 2000EP-0116126.  
XX PR 29-JUL-1999; 99JP-024036.  
XX PR 27-AUG-1999; 99JP-0300253.  
XX PR 11-JAN-2000; 2000JP-0118776.  
XX PR 02-MAY-2000; 2000JP-0182767.  
XX PR 09-JUN-2000; 2000JP-0241899.  
XX PA (HELI-) HELIX RES INST.  
XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
PI Ishii S, Sugiyama T, Wakanatsu A, Nagai K, Otsuki T;  
XX DR WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -  
XX PS Claim 1; SEQ ID 5321; 2537pp + CD ROM; English.  
XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dG primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH1633 to AAH18742 represent human cDNA sequences; AAH2446 to AAH3893 represent human amino acid sequences; and AAH1622 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX SQ Sequence 857 BP; 196 A; 235 C; 221 G; 201 T; 4 other;

Query Match 86.3%; Score 16.4; DB 22; Length 857; Best Local Similarity 94.4%; Pred. No. 3.3e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCTCTGATTCATGCTCTG 19  
Db 141 GCTCTGATTCATGCTCTG 158

RESULT 7

ABK94976  
ID ABK94976 standard; cDNA; 1769 BP.  
XX AC ABK94976;  
XX DT 30-AUG-2002 (first entry)  
XX DE Human novel polynucleotide #87.

XX Human; gene; ss; inflammatory condition; shock; sepsis; immune response; KW cancers; wound healing; central nervous system disease; haematoopoiesis; KW peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; KW cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; KW bone degenerative disorder; periodontal disease; reperfusion injury; KW lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; KW allergic condition; thrombolytic; thrombosis; coagulation disorder; KW fungal infection.  
XX OS Homo sapiens.  
XX PN WO2002443042.  
XX PD 06-JUN-2002.  
XX PR 30-NOV-2001; 2001WO-US47004.  
XX PR 30-NOV-2000; 2000US-0028952.  
XX PA (HYSEQ-) HYSEQ INC.

XX Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D; PT Yamazaki V, Ujwal ML, Drmanac RT;  
XX DR WPI; 2002-508509/54.  
XX DR P-PSDB, ABG66752.

XX Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -  
XX PS Claim 1; Page 546-548; 672pp; English.  
XX The invention relates to human novel polynucleotides and associated polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses

CC and cancer and for promoting wound healing. The sequences are used to CC induce the proliferation of neural cells and regeneration of nerve and CC brain tissue, and are useful for the treatment of central and peripheral CC nervous system diseases and neuropathies, such as Alzheimer's disease, CC Parkinson's disease, Huntington's disease and amyotrophic lateral CC sclerosis. The sequences are involved in chemotactic or chemokinetic CC activity, regulation of haemopoiesis, treatment of myeloid or lymphoid CC cell disorders and platelet disorders such as thrombocytopenia, CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal CC disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, CC reperfusion injury in various tissues, immune deficiencies and disorders CC including severe combined immunodeficiency (SCID), bacterial or fungal CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia gravis, allergic conditions such as asthma, thrombolytic drugs or thrombosis CC and coagulation disorders. Sequences ABK34890-ABK9482 represent human CC novel polynucleotides of the invention.

SQ Sequence 1769 BP; 389 A; 480 C; 483 G; 417 T; 0 other;

Query Match 86.3%; Score 16.4; DB 24; Length 1769;  
Best Local Similarity 94.4%; Pred. No. 3.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GCTGTGATTCCTGCTCTG 19  
Db 424 GCTGTGATTCCTGCTCTG 441

RESULT 8

AAH13643/c  
ID AAH13643 standard; cDNA; 1873 BP.  
XX  
AC AAH13643;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human cDNA sequence SEQ ID NO:10485.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000BP-0116126.  
XX  
PR 29-JUL-1999; 99JP-0248036.  
PR 27-AUG-1999; 99JP-030253.  
PR 11-JAN-2000; 2000JP-0118776.  
PR 02-MAY-2000; 2000JP-0183867.  
PR 09-JUN-2000; 2000JP-0241899.  
XX  
(HELI-) HELIX RES INST.

PA  
PI Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.;  
PI Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T.;  
XX  
DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 PT full-length cDNAs defined in the specification, and for the detection PT and/or diagnosis of the abnormality of the proteins encoded by the PT full-length cDNAs -  
XX  
PS Claim 8; SEQ ID 10485; 2537pp + CD ROM; English.  
XX  
CC The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary CC to the complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primer sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by CC the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13533 to AAH13742 represent human cDNA sequences; and ABP2446 to ABP9593 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification CC of the present invention.

SQ Sequence 1873 BP; 549 A; 419 C; 526 G; 379 T; 0 other;

Query Match 86.3%; Score 16.4; DB 22; Length 1873;  
Best Local Similarity 94.4%; Pred. No. 3.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GCTGTGATTCCTGCTCTG 19  
Db 914 GCTGTGATTCCTGCTCTG 897

RESULT 9

AAH16697  
ID AAH16697 standard; cDNA; 2252 BP.  
XX  
AC AAH16697;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human cDNA sequence SEQ ID NO:15859.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000BP-0116126.  
XX  
PR 29-JUL-1999; 99JP-0248036.  
PR 27-AUG-1999; 99JP-030253.  
PR 11-JAN-2000; 2000JP-0118776.  
PR 02-MAY-2000; 2000JP-0183867.  
PR 09-JUN-2000; 2000JP-0241899.  
XX  
(HELI-) HELIX RES INST.

PA  
PI Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.;  
PI Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K., Otsuki, T.;  
XX  
DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 PT full-length cDNAs defined in the specification, and for the detection PT and/or diagnosis of the abnormality of the proteins encoded by the PT full-length cDNAs -  
XX  
PS Claim 8; SEQ ID 10485; 2537pp + CD ROM; English.  
XX  
CC The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set

PR	24-FEB-2000;	2000WO-US05004.
CC	01-MAR-2000;	2000WO-US05001.
CC	20-MAR-2000;	2000WO-US05077.
CC	21-MAR-2000;	2000WO-US07332.
CC	30-MAR-2000;	2000WO-US08439.
PR	17-MAY-2000;	2000WO-US13705.
PR	22-MAY-2000;	2000WO-US14942.
PR	30-MAY-2000;	2000WO-US15264.
PR	02-JUN-2000;	2000WO-US15264.
PR	10-NOV-2000;	2000WO-US30873.
PA	XX	PA-PSDB; ARIU2201.
PT	XX	Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PT	XX	Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PT	XX	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
PI	XX	WPI; 2001-408281-43.
PI	XX	(GETH ) GENEWITCH INC.
CC	Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical -	
CC	Claim 3; Fig 59; 813PP; English.	
CC	CC AAS2124-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other CC PRO polypeptides to link bioactive molecules to cells expressing CC PRO polypeptides, to modulate biological activities of cells expressing CC PRO polypeptides, and to detect the presence of mammalian lung, colon, CC breast, prostate, rectal, cervical or liver tumours by comparing PRO CC polypeptide expression in cell sample to that in a control sample. CC Some of the 215 sequences are also useful to stimulate the release of CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the CC proliferation or differentiation of chondrocytes, the proliferation or CC gene expression in pericyte cells, the release of proteoglycans from CC cartilage, the proliferation of inner ear utricular supporting cells or CC of T-lymphocytes, the release of a cytokine from peripheral blood CC monocytes (PBMCS), or the proliferation of endothelial cells. Some of CC the PRO polypeptides may modulate glucose or free fatty acid uptake by CC skeletal muscle cells or by adipocytes, or inhibit binding of $\alpha$ -peptide CC to factor VIIIa. The PRO polypeptides can be used in assays to identify CC molecules involved in binding interactions. The antisense molecules encoding CC PRO polypeptides can be used to generate probes, antisense RNA/DNA, CC transgenic or knock out animals and can be used in gene therapy.	
CC	XX Sequence 2550 BP; 610 A; 666 C; 683 G; 591 T; 0 other;	
CC	CC Query Match Similarity 96.3%; Score 164; DB 22; Length 2550;	
CC	CC Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
CC	CC	
PR	01-DEC-2000; 2000WO-US32678.	
PR	XX	
PR	01-DEC-1999; 99WO-US38301.	
PR	01-DEC-1999; 99WO-US28634.	
PR	02-DEC-1999; 99WO-US28551.	
PR	02-DEC-1999; 99WO-US28564.	
PR	02-DEC-1999; 99WO-US28565.	
PR	09-DEC-1999; 99US-017062.	
PR	16-DEC-1999; 99WO-US0095.	
PR	20-DEC-1999; 99WO-US0911.	
PR	20-DEC-1999; 99WO-US3099.	
PR	30-DEC-1999; 99WO-US31243.	
PR	06-JAN-2000; 2000WO-US00277.	
PR	06-JAN-2000; 2000WO-US0376.	
PR	11-FEB-2000; 2000WO-US01565.	
PR	18-FEB-2000; 2000WO-US04341.	
PR	18-FEB-2000; 2000WO-US14342.	
PR	22-FEB-2000; 2000WO-US14414.	
PR	24-FEB-2000; 2000WO-US04914.	
DE	XX Human secreted protein gene #1.	
XX	XX Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; anti-rheumatic; dermatological; anti-proliferative; anti-arteriosclerotic; anticancer; pulmonary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis;	

KW multiple sclerosis; inflammatory disorder; inflammatory bowel disease;  
 KW Crohn's disease; nephritis; hyperproliferative disorder; haematoopoietic disorder;  
 KW cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer;  
 KW melanoma; lymphoma; wound healing; human; ss.  
 OS Homo sapiens.  
 XX WO20029435-A1.  
 XX  
 XX 25-MAY-2000.  
 XX  
 XX 27-OCT-1999; 99WO-US25031.  
 XX  
 XX 28-OCT-1998; 98US-0105971.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Ni, J., Ruben, SM., Olsen, HS., Young, PE., Kenny, JJ., Moore, PA., Wei, Y.;  
 PI Greene, J.M.;  
 DR WPI; 2000-307742/33.  
 DR P-PSDB; AAB25576.  
 XX  
 PT Isolated nucleic acid molecules encoding human secreted proteins are  
 PT used for the prevention, amelioration and treatment of autoimmune,  
 PT inflammatory, hyperproliferative and cardiovascular disorders, cancer,  
 PT wounds, and infectious diseases -  
 XX  
 PS Claim 1; Figure 1A-C; 803pp; English.  
 XX  
 CC The present invention relates to 12 secreted human proteins and the  
 CC nucleotide sequences encoding them. The polynucleotide sequences given  
 CC in AAB8006-A80623 encode the 12 secreted protein sequences given in  
 CC AAB25576-B25593. The human secreted proteins have various activities  
 CC dependent on the tissues in which they are expressed. Examples of the  
 CC activities of the proteins include: immunosuppressant;  
 CC anti-inflammatory; antiarthritic; antirheumatic; dermatological;  
 CC antiproliferative; anticancer; vulnery;  
 CC antiviral; antibacterial; and antifungal activity. The proteins,  
 CC polypeptides, agonists and antagonists may be used to treat, prevent  
 CC and/or diagnose various disease, disorders and conditions examples of  
 CC which include: immune disorders e.g. Addison's disease, rheumatoid  
 CC arthritis, dermatitis, and multiple sclerosis; inflammatory disorders  
 CC e.g. inflammatory bowel disease, Crohn's disease and nephritis;  
 CC hyperproliferative disorders such as paraproteinemias and purpura;  
 CC cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis;  
 CC cancer e.g. melanoma and lymphoma. The proteins and polynucleotide  
 CC sequences may also be used in wound healing and the treatment of  
 CC infectious diseases. The human secreted protein gene #1 and protein  
 CC sequences are represented in sequences AAB8006 and AAB25576. Also given  
 CC is an alternative protein product of human secreted protein gene #1 in  
 CC AAB25594.  
 XX  
 SQ Sequence 2609 BP; 682 A; 658 C; 680 G; 589 T; 0 other;  
 CC Query Match 86.3%; Score 16.4; DB 21; Length 2609;  
 CC Best Local Similarity 94.4%; Pred. No. 3.5e+02; Mismatches 17; Conservative 0; Indels 0; Gaps 0;  
 CC Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 QY 2 GCTTGATGCCGCTCG 19  
 DB 411 GCTTGATGACTGCTCG 428  
 RESULT 12  
 AAD05402/C  
 ID AAD05402 standard; cDNA; 3185 BP.  
 XX  
 AC AAD05402;  
 XX DT 17-JUL-2001 (first entry)  
 XX  
 DE Human secreted protein-encoding gene 14 cDNA clone HPUBK1, SEQ ID NO:24.

XX Human; secreted protein; proliferative disorder; cancer; tumour;  
 XX foetal abnormality; developmental abnormality; haematopoietic disorder;  
 XX immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 XX inflammation; allergy; neurological disorder; Alzheimer's disease;  
 XX Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 XX skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 XX cardiovascular disorder; angiogenic disorder; kidney disorder;  
 XX gastrointestinal disorder; infection; pregnancy-related disorder;  
 XX endocrine disorder; infection; wound healing; vulnery;  
 XX cell culture; chemotaxis; food additive; chromosome 9;  
 XX binding partner identification; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Ni, J., Ruben, SM., Olsen, HS., Young, PE., Kenny, JJ., Moore, PA., Wei, Y.;  
 PI Greene, J.M.;  
 DR WPI; 2001-3163577.  
 DR P-PSDB; AAB01559.  
 XX  
 PT 01-NOV-2000; 2000WO-US30037.  
 XX  
 PR 30-JUN-2000; 2000US-0215137.  
 PR  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PT Ruben, SM., Komatsoulis, GA., Moore, PA.;  
 PT DR WPI; 2001-3163590/33.  
 PT P-PSDB; AAB01559.  
 XX  
 PS Claim 1; Page 423-424; 535pp; English.  
 XX  
 CC AAB015389-AAB01543 represent cDNAs corresponding to 29 human secreted  
 CC protein genes, and AAB01546-AAB01630 represent the proteins they encode.  
 CC AAB01631-AAB01660 represent human secreted protein fragments or variants.  
 CC The secreted proteins and their genes are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the presence of  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 29 genes, based on the tissues in which they are most highly expressed,  
 CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental  
 CC abnormalities, haematopoietic disorders, diseases of the immune system,  
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC allergies, neurological disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and

CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein-encoding cDNA of the invention.  
 XX

SQ Sequence 3185 BP; 772 A; 808 C; 890 G; 715 T; 0 other;  
 Query Match 86.3%; Score 16.4; DB 22; Length 3185;  
 Best Local Similarity 94.4%; Pred. No. 3.6e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 GCTGTGATTCCTGCTCTG 19  
 Db 1515 GCTCAGATTCCTGCTCTG 1498

RESULT 13  
 ARQ8177/C  
 ID ARQ8177 standard; cDNA; 125439 BP.  
 XX  
 AC ABQ8177;  
 XX  
 DT 18-SEP-2002 (first entry)  
 XX  
 DR Human osteoblast differentiation related cDNA SEQ ID NO 84.  
 XX Human; osteoblast; stem cell differentiation; bone tissue deposition;  
 KW osteoporosis; osteopathic; ss.  
 XX  
 OS Homo sapiens.  
 XX WO20025301-A2.  
 XX PR 27-JUN-2002.  
 XX PP 18-DEC-2001; 2001WO-US48276.  
 XX PR 18-DEC-2000; 2000US-255892P.  
 XX PR 24-APR-2001; 2001US-285691P.  
 XX PA (GENE-) GENE LOGIC INC.  
 PA (PROC-) PROCTER & GAMBLE CO.  
 XX PI Jil D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;  
 PT Mertz L;  
 XX WPI; 2002-557663/59.  
 XX DR  
 PT Use of genes and their expression profiles associated with osteoblast  
 PT differentiation for screening modulators bone formation, for diagnosing  
 PT or treating e.g. osteoporosis, or as markers for the differentiation  
 PT process.  
 XX  
 PS Claim 1; SEQ ID NO 84; 78pp + Sequence Listing; English.  
 XX  
 CC The invention relates to genes and their expression profiles are used  
 CC for, screening modulators of precursor stem cell differentiation into  
 CC osteoblasts, or bone tissue deposition;  
 CC (b) diagnosing abnormal deposition of bone tissue, abnormal rate of  
 CC osteoblast formation or osteoporosis; or  
 CC (c) treating or monitoring treatment of the conditions cited in (b), or  
 CC monitoring the progression of bone tissue deposition.  
 CC Specific conditions include postmenopausal osteoporosis, glucocorticoid  
 CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy,  
 CC drug-induced abnormalities in bone formation or bone loss, conditions  
 CC that involve altered bone metabolism (e.g. idiopathic Juvenile  
 CC osteoporosis), skeletal disease linked to breast cancer, mastocytosis,  
 CC fibrous dysplasia. The present sequence is that of an  
 CC osteoblast differentiation associated cDNA marker of the invention.  
 Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at [ftp://wipo.int/pub/published/pct-sequences](http://wipo.int/pub/published/pct-sequences).  
 XX

RESULT 14  
 ABM45912/C  
 ID ABM45912 standard; DNA; 60 BP.  
 XX  
 AC ABM45912;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:18660.  
 KW Human; mouse; rat; splice transcript; detection; RNA transcript;  
 KW splice variant; transcriptome; Oligonucleotide library; ss.  
 XX OS Homo sapiens.  
 XX PR 20-JUL-2001; 2001WO-IB01903.  
 XX PR 28-JUL-2000; 2000US-221607P.  
 XX PR 02-MAY-2001; 2001US-287724P.  
 XX PD 07-FEB-2002.  
 XX PA (COMP-) COMPUGEN INC.  
 XX PT Shoshan A, Wasserman A, Mintz B, Mintz L, Faigler S;  
 PT XX DR WPI; 2002-257383/30.  
 XX PT New oligonucleotide libraries comprising oligonucleotides which  
 PT selectively hybridize to mRNAs transcribed from a transcription unit of  
 PT a genome, useful for detecting tissue-, pathology-, and  
 developmental-specific genes  
 XX PS Example 1; SEQ ID 18660; 47pp; English.  
 XX  
 CC The present invention describes oligonucleotide libraries for detecting  
 CC messenger RNAs that populate a (sub-)transcriptome, where the  
 CC (sub-)transcriptome comprises messenger RNAs transcribed from multiple  
 CC transcription units that populate a genome. The library comprises  
 CC several oligonucleotides, each capable of hybridising selectively to a  
 CC set of messenger RNAs transcribed from a given transcription unit of  
 CC the genome, which encodes one or more messenger RNA splice variants.  
 CC The oligonucleotide libraries are useful for detecting mRNAs from a  
 CC biological sample, in expression profiling studies, in qualitatively or  
 CC quantitatively characterising the corresponding transcriptome, and in  
 CC detecting RNA transcripts and splice variants of human or animal  
 CC transcripts. The libraries may also be used as specialised mini  
 CC libraries to detect transcripts of a sub-transcriptome under a  
 CC particular biological or pathological state, and so allowing the  
 CC detection of tissue- and pathology-specific genes such as those genes  
 CC only expressed in specific tissue under a specific pathological  
 CC condition; to detect developmental specific genes; and to detect RNA  
 CC transcripts and splice variants of a transcriptome of a patient suffering  
 CC from a particular disorder. ABM27353 to ABM5989 represent  
 CC oligonucleotide sequences from rats, humans and mice, which are used in  
 CC the exemplification of the present invention.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at [ftp://wipo.int/pub/published/pct-sequences](http://wipo.int/pub/published/pct-sequences).  
 XX

SQ Sequence 60 BP; 9 A; 17 C; 18 G; 16 T; 0 other;

Query Match 83.2%; Score 15.8; DB 24; Length 60;  
 Best Local Similarity 89.5%; Pred. No. 5.3e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgcctgtatccgcctgt 19  
 Db 50 CGCTAGATTCCTGCCNG 32

RESULT 15

ANT24088/c

ID ANT24088 standard; cDNA to mRNA; 151 BP.

XX

AC ANT24088;

XX

DT 06-SEP-1996 (first entry)

XX

DB Human gene signature HUMGS06076.

XX

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;

KW human; cloning; mapping; non-biased library; diagnosis; detection;

KW cell typing; abnormal cell function; ss.

XX

OS Homo sapiens.

XX

PN W09514772-A1.

XX

PD 01-JUN-1995.

XX

PP 11-NOV-1994; 94WO-JP01916.

XX

PR 12-NOV-1993; 93JP-0355504.

XX

PA (MATS/.) MATSUBARA K.

PA (OKUB/.) OKUBO K.

XX

PI Matsubara K, Okubo K;

XX

DR WPI; 1995-206931/27.

XX

PT Identifying gene signatures in 3'-directed human cDNA library - e.g.

PT for diagnosis of abnormal cell function, by preparing cDNA that

PT reflects relative abundance of corresp. mRNA in specific human

PT tissues

XX

PS Claim 1; Page 1527; 2245pp; Japanese.

XX

A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in ANT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.

DB 25 CACTAGAGATCTGAGCTG 7

Search completed: June 21, 2003, 19:39:34  
 Job time : 218 secs

Query Match 83.2%; Score 15.8; DB 16; Length 151;  
 Best Local Similarity 89.5%; Pred. No. 5.6e-02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGCTGATTCCTGCTCTG 19

GenCore version 5.1.6  
(c) 1993 - 2003 Compugen Ltd.

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

OM nucleic - nucleic search, using sw model  
Run on: June 21, 2003, 18:31:18 ; Search time 991 Seconds  
(without alignments)  
557.975 Million cell updates/sec

Title: US-09-581-500B-14

Perfect score: 19

Sequence: 1 cgctctgttccatgtctg 19

Scoring table: IDENTITY\_NUC

GapOp 10.0 , GapExt 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba: \*  
2: gb\_htg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_rn: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_uni: \*  
14: gb\_vl: \*  
15: em\_ba: \*  
16: em\_fun: \*  
17: em\_hum: \*  
18: em\_ini: \*  
19: em\_mui: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_pl: \*  
25: em\_rn: \*  
26: em\_sts: \*  
27: em\_vl: \*  
28: em\_vn: \*  
30: em\_htg\_hum: \*  
31: em\_htg\_inv: \*  
32: em\_htg\_other: \*  
33: em\_htg\_mus: \*  
34: em\_htg\_pln: \*  
35: em\_htg\_rdn: \*  
36: em\_htg\_mam: \*  
37: em\_htg\_vrt: \*  
38: em\_sy: \*  
39: em\_btgo\_hum: \*  
40: em\_btgo\_mus: \*  
41: em\_btgo\_other: \*

Result No.	Score	Query	Match	Length	DB	ID	Description
1	19	100.0	19	6	AX021008		AX021008 Sequence
2	19	100.0	656	6	AX021006		AX021006 Sequence
3	19	100.0	186351	2	AP001503	Homo sapi	AP001503 Homo sapi
4	19	100.0	191335	9	AC003802	Homo sapi	AC003802 Homo sapi
5	19	100.0	191793	2	AP001897	Homo sapi	AP001897 Homo sapi
6	19	100.0	198291	2	AC067875	Homo sapi	AC067875 Homo sapi
7	19	100.0	201734	2	AC090224	Homo sapi	AC090224 Homo sapi
8	17.4	91.6	2121	5	AF140243	Xenopus laevis	AF140243 Xenopus laevis
9	17.4	91.6	151130	2	AC127432	Mus musculus	AC127432 Mus musculus
10	17.4	91.6	151335	2	AC128860	Rattus norvegicus	AC128860 Rattus norvegicus
11	17.4	91.6	168369	2	AC111463	Rattus norvegicus	AC111463 Rattus norvegicus
12	17.4	91.6	176054	2	AC022377	Homo sapi	AC022377 Homo sapi
13	17.4	91.6	178548	2	AC018331	Homo sapi	AC018331 Homo sapi
14	17.4	91.6	189040	2	AC125748	Rattus norvegicus	AC125748 Rattus norvegicus
15	17.4	91.6	192180	2	AL84571	Mus musculus	AL84571 Mus musculus
16	17.4	91.6	196044	2	AC018505	Homo sapi	AC018505 Homo sapi
17	17.4	91.6	198597	2	AC026218	Homo sapi	AC026218 Homo sapi
18	17.4	91.6	198802	2	AC129207	Homo sapi	AC129207 Homo sapi
19	17.4	91.6	202844	2	AC090596	Homo sapi	AC090596 Homo sapi
20	17.4	91.6	203026	2	AL772271	Mus musculus	AL772271 Mus musculus
21	17.4	91.6	204412	2	AC021446	Mus musculus	AC021446 Mus musculus
22	17.4	91.6	205925	2	AC009111	Homo sapi	AC009111 Homo sapi
23	17.4	91.6	209876	2	AC011599	Homo sapi	AC011599 Homo sapi
24	17.4	91.6	229402	2	AC129177	Homo sapi	AC129177 Homo sapi
25	17.4	91.6	256657	2	AC090596	Homo sapi	AC090596 Homo sapi
26	17.4	91.6	203026	2	US8729		US8729
27	17.4	91.6	204412	2	HS110485		HS110485
28	17.4	91.6	205925	2	AC116868		AC116868
29	17.4	91.6	209876	2	AC068232		AC068232
30	17.4	91.6	229402	2	AP005230		AP005230
31	17.4	91.6	256657	2	AC068334		AC068334
32	17.4	91.6	208844	2	AC118200		AC118200
33	17.4	91.6	262387	2	AL670959		AL670959
34	17.4	91.6	305	11	AU027365		AU027365
35	16.4	86.3	502	6	AX079316		AX079316
36	16.4	86.3	511	6	AX079619		AX079619
37	16.4	86.3	540	8	CNS01818		CNS01818
38	16.4	86.3	901	11	CNS0884		CNS0884
39	16.4	86.3	1268	3	BC015201		BC015201
40	16.4	86.3	1873	9	AK00870		AK00870
41	16.4	86.3	2252	9	AK023902		AK023902
42	16.4	86.3	2343	9	BC034347		BC034347
43	16.4	86.3	2514	9	BC016552		BC016552
44	16.4	86.3	2550	6	AX63526		AX63526
45	16.4	86.3	2638	10	BC025476		BC025476

## ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

REFERENCE 1 (bases 1 to 19)  
AUTHORS Del-Favero,J., Raeymaekers,P. and Van Broeckhoven,C.  
TITLE Mood disorder gene  
JOURNAL Patent: WO 9932643-A 14 01-JUL-1999;





McEwan, P., McGurk, A., McKeenan, K., McSheeters, R., Medrim, J.,  
 Menous, L., Minova, T., Miranda, C., Mleenga, V., Morrow, J., Nayor, J.,  
 Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T.M.,  
 Peterson, K., Pierre, M., Pissani, C., Pollara, V., Raymond, C.,  
 Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,  
 Severy, P., Spencer, B., Stanger-Thomann, N., Storanovic, N.,  
 Subramanian, A., Talamas, J., Tasfave, S., Theodore, J., Tirrell, A.,  
 Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vol, A., Wilson, B.,  
 Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and  
 Zody, M.

TITLE Direct submission  
 JOURNAL Submitted (17-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141 USA  
 COMMENT On Jan 16, 2000 this sequence version replaced g1:6514043.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RW/RepeatMasker.html>

Center: Whitehead Institute/ MIT center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

Center project name: L1250

Center clone name: 793\_J\_2

FEATURES location/Qualifiers

SOURCE

1. .1911395  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="18"  
 /map="1"  
 /rpt\_family="L1PA16"  
 /clone\_id="RPT1-793J2"  
 repeat\_region  
 2. .542  
 /rpt\_family="L1M21"  
 /clone\_id="RPTCI-11 Human Male BAC"  
 repeat\_region  
 474. .708  
 /rpt\_family="L1"  
 repeat\_region  
 708. .1353  
 /rpt\_family="L1"  
 repeat\_region  
 1351. .1623  
 /rpt\_family="L1MA4A"  
 repeat\_region  
 1632. .1687  
 /rpt\_family="TATATG1"  
 complement(1673. .1726)  
 /note="Single-stranded coverage."  
 repeat\_region  
 1688. .2207  
 /rpt\_family="L1MA4A"  
 complement(1724. .1770)  
 /note="Single-stranded terminator coverage."  
 repeat\_region  
 2208. .2215  
 /rpt\_family="TATATG1"  
 repeat\_region  
 2594. .2648  
 /rpt\_family="L1ME"  
 repeat\_region  
 2992. .3475  
 /rpt\_family="MER2"  
 repeat\_region  
 4982. .5151  
 /rpt\_family="FRAM"  
 repeat\_region  
 4438. .4567  
 /rpt\_family="TATA1"  
 repeat\_region  
 4599. .4959  
 /rpt\_family="AT\_Rich"  
 repeat\_region  
 5144. .5311  
 /rpt\_family="TATTCG1"  
 repeat\_region  
 5257. .5441  
 /rpt\_family="TATA1"  
 repeat\_region  
 5444. .5525  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 5533. .5708

repeat\_region  
 /rpt\_family="TTATA1"  
 5742. .5507  
 /rpt\_family="TTATA1"  
 complement(5566. .6047)  
 /rpt\_family="FRAM/FAM"  
 repeat\_region  
 6682. .6703  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 7034. .7933  
 /rpt\_family="L1PA16"  
 repeat\_region  
 7935. .8006  
 /rpt\_family="AluY"  
 repeat\_region  
 8009. .9111  
 /rpt\_family="L1PA16"  
 9112. .9165  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 9216. .9496  
 /rpt\_family="AluX"  
 repeat\_region  
 9497. .9550  
 /rpt\_family="CAAA1"  
 9561. .10364  
 /rpt\_family="L1PA16"  
 complement(10837. .10840)  
 /note="Single-stranded terminator coverage."  
 repeat\_region  
 11856. .11987  
 /rpt\_family="MIR"  
 repeat\_region  
 12592. .12643  
 /rpt\_family="L12"  
 repeat\_region  
 13683. .13994  
 /rpt\_family="AluX"  
 repeat\_region  
 14788. .15255  
 /rpt\_family="L1MEC"  
 repeat\_region  
 15101. .15135  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 16136. .16304  
 /rpt\_family="L1M4"  
 complement(16572. .16647)  
 /rpt\_family="AluY"  
 complement(16716. .17011)  
 /rpt\_family="MER67D"  
 /rpt\_family="MER5B1"  
 complement(15996. .15160)  
 /rpt\_family="MER5B1"  
 repeat\_region  
 18222. .18755  
 /rpt\_family="AluY"  
 repeat\_region  
 17827. .17939  
 /rpt\_family="L1ME3"  
 complement(17945. .18133)  
 /rpt\_family="MER50A"  
 repeat\_region  
 1883. .19019  
 /rpt\_family="L1ME3"  
 repeat\_region  
 19573. .19616  
 /rpt\_family="CAGCG1"  
 repeat\_region  
 20506. .20544  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 21894. .22184  
 /rpt\_family="AluSQ"  
 complement(22187. .22398)  
 /rpt\_family="TR40a"  
 complement(23074. .23133)  
 /rpt\_family="L1TR40b"  
 repeat\_region  
 23184. .23540  
 /rpt\_family="L12"  
 complement(23675. .25225)  
 /rpt\_family="PTRS5"  
 repeat\_region  
 25229. .25582  
 /rpt\_family="THE1B"  
 repeat\_region  
 25875. .26031  
 /rpt\_family="MT111"



4574 53200: contig of 7457 bp in length  
 \* 53301 53300: gap of 100 bp  
 \* 53401 59466: contig of 6166 bp in length  
 \* 53467 59565: gap of 100 bp  
 \* 53667 63023: contig of 5457 bp in length  
 \* 65124 65123: gap of 100 bp  
 \* 65124 71725: contig of 6602 bp in length  
 \* 71226 71825: gap of 100 bp  
 \* 71826 77046: contig of 5221 bp in length  
 \* 77047 77146: gap of 100 bp  
 \* 77147 82059: contig of 4913 bp in length  
 \* 82050 82159: gap of 100 bp  
 \* 82160 86515: contig of 4356 bp in length  
 \* 86516 86615: gap of 100 bp  
 \* 86616 98836: contig of 4221 bp in length  
 \* 90337 90938: gap of 100 bp  
 \* 90337 95257: contig of 4321 bp in length  
 \* 92458 92276: contig of 3919 bp in length  
 \* 92458 92276: gap of 100 bp  
 \* 99277 99375: gap of 100 bp  
 \* 99377 103751: contig of 4375 bp in length  
 \* 103752 103851: gap of 100 bp  
 \* 103852 108407: contig of 4556 bp in length  
 \* 108408 108507: gap of 100 bp  
 \* 112468 112468: contig of 3961 bp in length  
 \* 112469 112508: gap of 100 bp  
 \* 112469 116411: contig of 3843 bp in length  
 \* 116411 116511: gap of 100 bp  
 \* 116512 120690: contig of 4179 bp in length  
 \* 120591 120791: gap of 100 bp  
 \* 120791 125789: contig of 4999 bp in length  
 \* 125790 125809: gap of 100 bp  
 \* 125809 128429: contig of 3540 bp in length  
 \* 129430 129529: gap of 100 bp  
 \* 129530 130875: contig of 3346 bp in length  
 \* 132076 132976 135718: gap of 100 bp  
 \* 136813 136819: gap of 100 bp  
 \* 136819 140204: contig of 3386 bp in length  
 \* 140205 140304: gap of 100 bp  
 \* 140305 142121: contig of 2908 bp in length  
 \* 143213 143312: gap of 100 bp  
 \* 143313 143311: contig of 2999 bp in length  
 \* 146112 146411: gap of 100 bp  
 \* 146412 148694: contig of 2283 bp in length  
 \* 148695 148794: gap of 100 bp  
 \* 148795 151551: contig of 2757 bp in length  
 \* 151552 151552: gap of 100 bp  
 \* 153472 153571: contig of 1820 bp in length  
 \* 153572 153505: contig of 2334 bp in length  
 \* 155906 156005: gap of 100 bp  
 \* 156006 157930: contig of 1925 bp in length  
 \* 157931 158030: gap of 100 bp  
 \* 158031 160335: contig of 2305 bp in length  
 \* 160436 160455: gap of 100 bp  
 \* 160436 161957: contig of 1522 bp in length  
 \* 161958 162057: gap of 100 bp  
 \* 162058 164115: contig of 2058 bp in length  
 \* 164115 164215: gap of 100 bp  
 \* 164216 166374: contig of 2159 bp in length  
 \* 166375 166741: gap of 100 bp  
 \* 166475 168634: contig of 2160 bp in length  
 \* 168635 168734: gap of 100 bp  
 \* 168735 170796: contig of 2062 bp in length  
 \* 170797 170897: gap of 100 bp  
 \* 172732 172831: contig of 1835 bp in length  
 \* 172832 174464: contig of 1533 bp in length  
 \* 174465 174564: gap of 100 bp  
 \* 174565 175580: contig of 1116 bp in length  
 \* 175581 175780: gap of 100 bp  
 \* 175781 176918: contig of 1138 bp in length

RESULT 6  
 AC067875 LOCUS AC067875  
 DEFINITION Homo sapiens chromosome 18 clone RP11-589E3 map 18, \*\*\* SEQUENCING  
 ACCESION AC067875  
 VERSION AC067875.7 GI:14193020  
 KEYWORDS HTGS PHASE1; HTGS\_FULLTOP; HTGS\_ACTIVEFIN.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 192891)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barra, N., Bastien, V., Beda, F., Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 TITLE Homo sapiens chromosome 18, clone RP11-589E3  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 198291)  
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Gindre, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Haggas, B., Heaford, A., Horton, J., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kahn, L., Karatsis, A., Boguila, V., Boukiga, J., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepe, P., Colangelo, M., Collins, S., Colmbo, A., Cooke, P., Dearlano, K., Dewart, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzgerald, W., Gage, D., Galagan, J., Gardyn, S., Ginde, S., Govert, M., Graham, L., Meldrim, J., Meneus, R., Minova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Poliara, V., Raymond, C., Riley, R., Rodov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Strange, M., Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Turrell, A., Travers, M., Trigilio, J., Vassiliev, H., Vial, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.  
 TITLE JOURNAL  
 COMMENT Submitted (27-APR-2000) Whithead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On May 24, 2001 this sequence version replaced gi:13560423.  
 All repeats were identified using RepeatMasker: 1.0.0 (1996-1997)  
 Smit, A.F.A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html  
 Center: Whitehead Institute/ MIT Center for Genome Research  
 Center code: WIBR  
 Web site: http://www-seq.wi.mit.edu  
 Contact: sequence\_submissions@genome.wi.mit.edu  
 ----- Project Information  
 Center project name: l8557  
 Center clone name: l859\_E\_3  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence.



RESULT 8

Query Match 100.0%; Score 19; DB 2; Length 201734; Best Local Similarity 100.0%; Pred. No. 20; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; FNG 0

QY 1 CGCTCTGATCCCTGCTG 19

Db 147537 CGCTCTGATCCCTGCTG 147555

ACI140243/C

DEFINITION Xeno<sup>1</sup>ps laevis axin-related protein mRNA, complete cds.

ACCESSION ACI140243

VERSION ACI140243.1 GI:6652990

KEYWORDS XENOPUS LAEVIS

SOURCE XENOPUS LAEVIS

ORGANISM XENOPUS LAEVIS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus

REFERENCE 1 (bases 1 to 2121)

AUTHORS Itoh,K., Antipova,A., Ratcliffe,M.J. and Sokol,S.

TITLE Interaction of dishevelled and Xenopus axin-related protein is required for wnt signal transduction

JOURNAL Mol. Cell. Biol. 20 (6), 2228-2238 (2000)

PMID 1068869

2 (bases 1 to 2121)

AUTHORS Antipova,A., Itoh,K. and Sokol,S.

TITLE Submitted (02-APR-1999) Microbiology and Medical Genetics, Harvard Medical School, BIMC, East Campus, RW663, 330 Brookline Avenue, Boston, MA 02215, USA

JOURNAL Location/Qualifiers

FEATURES source

1. 2121 /organism="Xenopus laevis"

/db\_xref="taxon:8355"

2. 2121 /tissue\_type="ovary"

3. 2121 /note="ARP"

/codon\_start=1

/product="xin-related protein"

/protein\_id="AAF22574.1"

/db\_xref="GI:6652991"

/translation="MSAAGVLTCDPDSPIRETSLRPPVPGOETNNPKPEKPTMDQHKKEDPRNREAGVWAHSRSRSGNSLNLDDGATLFRNLEGGGLDITPFAKGFFAMDLIEPKVSKKAKAYWVYNSAVSRKPTKTRVQKCVKHQKLTWVDOAQETDAMOBATFQDCKYRGVSDPPEPSGCPGKDFDDEPQGKLFHFSSEMGKRNRAKSRPFRNQSHFRRKLTQVAFASINDESSDALTEDSMWTDGSDTGUPTPYRKKQHRSVHSANGKVSUPLVPTWRPABMTPSPRFKATTALEKUKKQDAAERKLCEPLQADYDIPSSHETVEGALVEDDQSTIDDHVSRLKTPAMLPQSOSFVORKGKFOFAPSKQGPTSTSRKLRVKFQMEBISTASAKMKKHFERASVPCPHEKRAASPHRLQDTPSMPPATDOLBEEARLVEDKRVKHKRSVOSTLKEKGKAAESPSSGFSITKLSHQKAKKSSCPGQSGIAIVYVFCRIPPMIRKERSLTIQEFKLLSKRGSKNKKYHKESHEFCNAVQFQEVSEEDAVLPFLERKICKERSLTIQEFKLLSKRGSKNKKYHKESHEFCNAVQFQ

BASE COUNT 637 a 501 c 507 g 476 t

ORIGIN

Query Match 91.6%; Score 17.4; DB 5; Length 2121; Best Local Similarity 94.7%; Pred. No. 1.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0; FNG 0

QY 1 CGCTCTGATCCCTGCTG 19

Db 1490 CGCTCTGATCCCTGCTG 1472

ACI124432

DEFINITION Mus musculus clone RP24-535L6, complete sequence.

ACCESSION ACI124432

VERSION ACI124432.1 GI:21844636

KEYWORDS house mouse

SOURCE Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Muzinae; Mus

REFERENCE 1 (bases 1 to 151130)

AUTHORS McPherson,J.D. and Waterston,R.H.

TITLE The sequence of Mus musculus clone Unpublished

JOURNAL 2 (bases 1 to 151130)

COMMENT Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site:<http://genome.wustl.edu/gsc/index.shtml>

Contact: [submissions@wustl.wustl.edu](mailto:submissions@wustl.wustl.edu)

----- Project Information -----

Center project name: M BB0335L6

Parkway, St. Louis, MO 63108, USA

RESULT 9

Query Match 91.6%; Score 17.4; DB 5; Length 2121; Best Local Similarity 94.7%; Pred. No. 1.3e+02; Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0; FNG 0

QY 1 CGCTCTGATCCCTGCTG 19

Db 99788 CGCTCTGATCCCTGCTG 99806

ACI128860

DEFINITION Rattus norvegicus clone CH230-43707, \*\*\* SEQUENCING IN PROGRESS

ACCESSION ACI128860

VERSION ACI128860.1 GI:21952979

KEYWORDS HTGS, HTGS PHASEL

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus

REFERENCE 1 (bases 1 to 151395)

AUTHORS Murzy,D.M., Adams,C., Adio-odulua,B., Ali-osman,F.R., Allen,C., Alshrookh,S.I., Amaratunge,H.C., Ar,J.R., Ayle,M., Banks,T., Barabria,J., Benton,J., Bimber,K., Blankenburg,K., Bonnin,D., Bouch,J., Bowie,S., Briva,M., Brown,B., Brown,M., Bryant,N.P., Buncy,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davilla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.H.A., Delaney,K.R., Delgado,O., Dunn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Barnhart,C., Edgar,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Falls,T., Ferragudo,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,

RESULT 9

Correll,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., \*  
 Harris,C., Harris,K., Hart,M., Havlik,P., Hayes,A., Hernandez,J., \*  
 Hernandez,O., Hodges,A., Hogues,M., Holloway,C., Hollins,B., \*  
 Homsi,F., Howard,S., Huber,J., Huijts,S., Hume,J., Jackson,L.E., \*  
 Jacobson,B., Jia,Y., Johnson,R., Jolyer,S., Joudah,S., \*  
 Karlsson,E., Kelli,S., Khan,U., King,J., Kovari,J., Kovar,C., \*  
 Kratoric,J., Kureishi,A., Landy,N., Leal,B., Lewis,L.C., Lewis,L., \*  
 Li,J., Li,Z., Licharge,O., Liou,C., Liu,J., Liu,W., Louiseged,H., \*  
 Iozado,R.J., Lu,X., Lucier,A., Lucier,R., Luns,R., Ma,J., \*  
 Maseshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., \*  
 Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mai,G., Metzker,M., \*  
 Miner,G., Miner,Z., Mitchell,T., Mohabat,K., Morgan,M., Morris,S., \*  
 Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., \*  
 Nguyen,N., Nickeron,E., Nwoekwo,S., Oguri,M., Okwouo,G., \*  
 Oragunye,N., Oviado,R., Pace,A., Payton,B., Peery,J., Perez,L., \*  
 Peters,L., Pickens,R., Primus,R., Pu,L.L., Quiles,M., Ren,Y., \*  
 Rives,M., Rojas,A., Rejoubi,I., Roife,M., Ruiz,S., Savery,G., \*  
 Scherer,S., Scott,G., Shen,H., Shooshani,N., Sisson,I., \*  
 Soderren,F., Sonnike,T., Sparks,A., Stanley,H., Stone,H., \*  
 Sutton,A., Svatek,A., Tabor,P., Tamersa,A., Tang,H., \*  
 Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., \*  
 Usmani,K., Vasquez,J., Vera,V., Villaon,D., Vinson,R., Wang,Q., \*  
 Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., \*  
 Williams,G., Williamson,A., Wleczik,R., Wooden,S., Worley,K., \*  
 Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., \*  
 Weinstock,G., and Gibbs,R.  
 Direct submission  
 JOURNAL  
 AUTHORS  
 TITLE  
 JOURNAL  
 REFERENCE  
 COMMENT  
 -----  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 -----  
 Center project name: KAWI  
 Center clone name: CH220-43707  
 -----  
 Summary Statistics  
 Sequencing vector: Plasmid;  
 Chemistry: Dye-terminator Big Dye: 100% of reads  
 Assembly program: Phrap; version 0.99029  
 Consensus quality: 88.95 bases at least Q40  
 Consensus Quality: 94037 bases at least Q30  
 Consensus quality: 97692 bases at least Q20  
 -----  
 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 62 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1. 1380: contig of 1380 bp in length  
 \* 1381: 1480: gap of unknown length  
 \* 1481: 2902: contig of 1422 bp in length  
 \* 2903: 3002: gap of unknown length  
 \* 3003: 4595: contig of 1593 bp in length  
 \* 4596: 4696: gap of unknown length  
 \* 4696: 6308: contig of 1613 bp in length  
 \* 6309: 6408: gap of unknown length  
 \* 6409: 8011: contig of 1603 bp in length  
 \* 8012: 8112: gap of unknown length  
 \* 8112: 9345: contig of 1234 bp in length  
 \* 9346: 9445: gap of unknown length  
 \* 9446: 10512: contig of 1067 bp in length

10513: 10612: gap of unknown length  
 10613: 10823: contig of 1211 bp in length  
 11824: 11923: gap of unknown length  
 11924: 11924: contig of 1699 bp in length  
 13623: 13722: gap of unknown length  
 13723: 14750: contig of 1028 bp in length  
 14751: 14850: gap of unknown length  
 14851: 16300: contig of 1450 bp in length  
 16301: 16400: gap of unknown length  
 16401: 18220: contig of 1820 bp in length  
 18221: 18320: gap of unknown length  
 18321: 20138: contig of 1818 bp in length  
 20139: 20238: gap of unknown length  
 20239: 21481: contig of 1242 bp in length  
 21481: 21580: gap of unknown length  
 21581: 22983: contig of 1403 bp in length  
 22983: 22984: gap of unknown length  
 22984: 24507: contig of 1424 bp in length  
 24508: 24607: gap of unknown length  
 24607: 26477: contig of 1770 bp in length  
 26477: 26478: gap of unknown length  
 26478: 27917: contig of 1440 bp in length  
 27917: 28018: gap of unknown length  
 28018: 29273: contig of 1256 bp in length  
 29273: 29373: gap of unknown length  
 29373: 29374: contig of 1769 bp in length  
 29374: 31143: gap of unknown length  
 31143: 31242: gap of unknown length  
 31243: 32285: contig of 1043 bp in length  
 32285: 32386: gap of unknown length  
 32386: 33650: contig of 1265 bp in length  
 33650: 33751: gap of unknown length  
 33751: 36212: contig of 2126 bp in length  
 36212: 36312: gap of unknown length  
 36312: 37975: contig of 1663 bp in length  
 37975: 37976: gap of unknown length  
 37976: 38075: contig of 1137 bp in length  
 38075: 38076: contig of 2101 bp in length  
 38076: 40176: contig of 1137 bp in length  
 40176: 40276: gap of unknown length  
 40276: 40377: contig of 2126 bp in length  
 40377: 42502: gap of unknown length  
 42502: 42603: contig of 1347 bp in length  
 42603: 42824: gap of unknown length  
 42824: 43194: contig of 1407 bp in length  
 43194: 43350: gap of unknown length  
 43350: 45086: contig of 1137 bp in length  
 45086: 45186: gap of unknown length  
 45186: 45277: contig of 1541 bp in length  
 45277: 46728: gap of unknown length  
 46728: 46827: gap of unknown length  
 46827: 48234: contig of 1407 bp in length  
 48234: 48334: gap of unknown length  
 48334: 49955: contig of 1621 bp in length  
 49955: 50056: gap of unknown length  
 50056: 52476: contig of 2421 bp in length  
 52476: 52577: gap of unknown length  
 52577: 54207: contig of 2331 bp in length  
 54207: 54907: gap of unknown length  
 54907: 55001: contig of 2100 bp in length  
 55001: 55508: 57389: contig of 2382 bp in length  
 57389: 57579: gap of unknown length  
 57579: 57930: gap of unknown length  
 57930: 57949: contig of 2530 bp in length  
 57949: 60119: gap of unknown length  
 60119: 60220: contig of 2100 bp in length  
 60220: 62219: gap of unknown length  
 62219: 62319: gap of unknown length  
 62319: 62320: 64250: contig of 1931 bp in length  
 64250: 64350: gap of unknown length  
 64350: 64421: gap of unknown length  
 64421: 65981: contig of 1639 bp in length  
 65981: 66089: gap of unknown length  
 66089: 66090: 68073: contig of 1984 bp in length  
 68073: 68074: gap of unknown length  
 68074: 68174: 70180: contig of 2007 bp in length  
 70180: 70280: gap of unknown length  
 70280: 70281: contig of 1906 bp in length  
 70281: 72187: 72286: gap of unknown length  
 72286: 74046: contig of 1760 bp in length  
 74046: 74147: 76610: contig of 2464 bp in length  
 76610: 76710: gap of unknown length



9703 9802: gap of unknown length  
 \* 11137: contig of 1335 bp in length  
 \* 11138 11237: gap of unknown length  
 \* 11238 12257: contig of 1020 bp in length  
 \* 12258 12357: gap of unknown length  
 \* 12355: contig of 1598 bp in length  
 \* 12356 13055: gap of unknown length  
 \* 13056 13937: contig of 1882 bp in length  
 \* 13937: gap of unknown length  
 \* 16038 17076: contig of 1669 bp in length  
 \* 17077 17806: gap of unknown length  
 \* 17807 19352: contig of 1546 bp in length  
 \* 19353 19452: gap of unknown length  
 \* 19453 20883: contig of 1431 bp in length  
 \* 20883: gap of unknown length  
 \* 20884 20848: contig of 1065 bp in length  
 \* 22144: gap of unknown length  
 \* 22149 22896: contig of 1748 bp in length  
 \* 23397 23996: gap of unknown length  
 \* 23997 25355: contig of 1360 bp in length  
 \* 25357 25456: gap of unknown length  
 \* 25457 26764: contig of 1308 bp in length  
 \* 26765 26864: gap of unknown length  
 \* 26865 26982: contig of 1118 bp in length  
 \* 27783 28083: gap of unknown length  
 \* 29140: contig of 1058 bp in length  
 \* 29240: gap of unknown length  
 \* 29241 30671: contig of 1431 bp in length  
 \* 30672 30771: gap of unknown length  
 \* 32820: contig of 2049 bp in length  
 \* 32921 33405: gap of unknown length  
 \* 33406 34505: gap of unknown length  
 \* 34506 36497: contig of 1992 bp in length  
 \* 36498 36598: contig of 1039 bp in length  
 \* 37637 37736: gap of unknown length  
 \* 37737 39116: contig of 1580 bp in length  
 \* 39317 39416: gap of unknown length  
 \* 39417 40439: contig of 1023 bp in length  
 \* 40440 40539: gap of unknown length  
 \* 40540 41568: contig of 1029 bp in length  
 \* 41569 41668: gap of unknown length  
 \* 41669 42719: contig of 1051 bp in length  
 \* 42720 42819: gap of unknown length  
 \* 42820 44594: contig of 1775 bp in length  
 \* 44595 44694: gap of unknown length  
 \* 44695 45911: contig of 1217 bp in length  
 \* 45912 46011: gap of unknown length  
 \* 46012 47510: contig of 1499 bp in length  
 \* 47511 47610: gap of unknown length  
 \* 47611 48721: contig of 1111 bp in length  
 \* 48722 48821: gap of unknown length  
 \* 48822 50922: contig of 2101 bp in length  
 \* 51022: gap of unknown length  
 \* 51023 52233: contig of 1211 bp in length  
 \* 52234 52333: gap of unknown length  
 \* 52334 54084: contig of 1751 bp in length  
 \* 54085 55537: contig of 1355 bp in length  
 \* 55538 55537: gap of unknown length  
 \* 55638 55748: contig of 1611 bp in length  
 \* 55749 55348: gap of unknown length  
 \* 57349 59510: contig of 2162 bp in length  
 \* 59511 59611: gap of unknown length  
 \* 59611 60612: contig of 1002 bp in length  
 \* 60613 60713: gap of unknown length  
 \* 62445 62545: gap of unknown length  
 \* 62546 64953: contig of 1508 bp in length  
 \* 64054 66613: gap of unknown length  
 \* 66614 67113: gap of unknown length

Query Match 91.6%; Score 17.4; DB 2; Length 168369;  
 Best Local Similarity 94.7%; Prc. No. 1.5e-02; Mismatches 1; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 CGCTCTGATTCTGCTCTG 19  
 Db 4044 CGCTCTGATTCTGCTATG 4026

85136 85036 85035: contig of 1376 bp in length  
 85136 85036 85035: gap of unknown length  
 85136 85136 87276: contig of 2141 bp in length

RESULT 12

AC022377 LOCUS AC022377 176054 bp DNA linear RING 12-OCT-2000  
 DEFINITION Homo sapiens chromosome 3, WORKING DRAFT SEQUENCE. 6 unordered  
 pieces.

AC022377 VERSION AC022377.2 GI:10305054  
 KEYWORDS HG3; HTGS\_PHASE1; HTGS\_DRAFT.

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelesostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 176054)  
 AUTHORS Lin,W., Zhang,C., Dong,H., Wan,M., Xu,S., Gu,W., Tu,Y., Jia,J.,  
 Wu,C., Lu,G., Zhong,M., Zhou,Y., Ren,S., Fu,G., Chen,Z. and  
 Huang,M.

TITLE JOURNAL Submitted (03-FEB-2000) Genomic Dept., Chinese National Human  
 Genome Center at Shanghai, 315 Guo Shou Jing Road, Shanghai,  
 Shanghai, 201203, P. R. China

COMMENT On Sep 26, 2000 this sequence version replaced gi:6862623.  
 ----- Genome Center-----  
 Center:Beijing Center  
 Center code:Beijing  
 Website: <http://hgc.igtp.ac.cn>  
<http://www.genomics.org.cn>  
 Contact:hgc@igtp.ac.cn

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 6 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 8523: contig of 8523 bp in length  
 \* 8524 21709: contig of 1318 bp in length  
 \* 21710 39761: contig of 18052 bp in length  
 \* 39762 42545: contig of 2784 bp in length

FEATURES	*	42546	96169:	gap of unknown length	Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
	*	42546	96169:	conig of 53624 bp in length	100101, P.R.China
	*	42546	96169:	gap of unknown length	On Feb 9, 2001 this sequence version replaced gi:6862651.
FEATURES	*	96170	176054:	conig of 79885 bp in length.	-----Genome Center
FEATURES	*	96170	176054:	Location/Qualifiers	Center:Beijing Center
FEATURES	*	96170	176054:	1.-176054	Center code:Beijing
FEATURES	*	96170	176054:	/organism="Homo sapiens"	Website: <a href="http://hgcc.igtp.ac.cn">http://hgcc.igtp.ac.cn</a>
FEATURES	*	96170	176054:	/db_xref="taxon:9606"	<a href="http://www.genomics.org.cn">http://www.genomics.org.cn</a>
FEATURES	*	96170	176054:	/clone_id="481b18"	Contact: <a href="mailto:igcc@igtp.ac.cn">igcc@igtp.ac.cn</a>
BASE COUNT	40089	a	47246	c 47642	-----Project Information
ORIGIN					Center project name:1% project
ORIGIN					Center clone name:RP11-481B18
ORIGIN					-----Summary Statistics
ORIGIN					Sequencing vector:pUC18; 10% of reads
ORIGIN					Chemistry: Dye-terminator; ET 55% of reads
ORIGIN					Chemistry: Dye-terminator Big Dye; 45% of reads
ORIGIN					Assembly program: Phrap; version 0.990329
ORIGIN					Consensus quality: 182029 bases at least 040
ORIGIN					Consensus quality: 182113 bases at least 030
ORIGIN					Consensus quality: 182119 bases at least 020
ORIGIN					Insert size: 17858; sum-of-contigs
ORIGIN					Quality coverage: 15.40x in Q20 bases;sum-of-contigs
RESULT	13				-----
AC018831/c					-----
LOCUS	AC018831		178548	bp	-----
DEFINITION	Homo sapiens chromosome 3 clone RP11-481B18 map 3p, complete				-----
ACCESSION	AC018831				-----
VERSION	AC018831.4				-----
KEYWORDS	HTG				-----
SOURCE	Homo sapiens.				-----
ORGANISM	Homo sapiens.				-----
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				-----
AUTHORS	Li,F., Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J and Yang,H.				-----
TITLE	Chromosome 3p genomic sequence				-----
JOURNAL	Unpublished				-----
REFERENCE	2 (bases 1 to 178548)				-----
AUTHORS	Zeng,Y., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Niu,Y., Bao,N., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Bao,J., Bao,Q., Bao,J., Wang,Y., Zhang,X., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L., Feng,X., Wang,X., Yu,J and Yang,H.				-----
REFERENCE	Submitted (21-DEC-1999) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing				-----
REFERENCE	3 (bases 1 to 178548)				-----
AUTHORS	Li,F., Bao,J., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y., Luo,J., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L., Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J., Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X., Wu,D., Wu,Q., Xie,F., Xuan,Z., Xue,Y., Yan,C., Yang,X., Yu,B., Zeng,Y., Zhang,G., Zhang,H., Zhang,H., Zhang,L., Zhang,M., Zhang,X., Zhang,X., Zhang,Y., Zhang,Y., Zhang,Z., Zhu,B., Zhu,N., Yu,J and Yang,H.				-----
REFERENCE	Direct Submission				-----
JOURNAL	Submitted (09-FEB-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing				-----
COMMENT	On Feb 9, 2001 this sequence version replaced gi:6862651.				-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a	46869	c 49493	-----
ORIGIN	AC125748		42580	t	-----
FEATURES	*	60286	178548	bp	-----
BASE COUNT	39606	a			





/note="assembly fragment:01782  
fragment chain:1  
clone\_end:17  
vector side:right"

BASE COUNT 46064 a 48223 c 48472 g 46190 t 1225 others  
ORIGIN

Query Match 91.5%; Score 17.4; DB 2; length 192180;  
Best Local Similarity 94.7%; Pred. No. 1.5e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CGCTCGATTCCTGCTG 19  
Db 27976 CGCTCTGATTCCTGCCCTG 27994

Search completed: June 21, 2003, 19:56:22  
Job time : 997 secs